ACCESS DB # _____

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 11-8-06
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/719,370
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): (PAPER) DISK
****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: AS modrag HIF1

Inventors (please provide full names): Ward et al

Earliest Priority Date: 11-21-03

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only ***Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.***

Please Search Seq ID No: 446

Size limit 8 - 30 NT's.

please do a Score over length Search.

Limit to 70% IDENTITY or greater.

THANKS

****

STAFF USE ONLY

Searcher: _____
Searcher Phone #: _____
Searcher Location: _____
Date Searcher Picked Up: _____
Date Completed: _____
Searcher Prep & Review Time: _____
Online Time: _____

Type of Search

_____ NA Sequence (#)
_____ AA Sequence (#)
_____ Structure (#)
_____ Bibliographic
_____ Litigation
_____ Fulltext
_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog
_____ Questel/Orbit _____ Lexis/Nexis
_____ Westlaw _____ WWW/Internet
____ In-house sequence systems
__ Commercial ___ Oligomer ____ Score/Length
__ Interference ___ SPDI ____ Encode/Transl
_____ Other (specify)

11/22/06
10/719370
SEQ 446

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 14:05:02 ; Search time 0.001 Seconds
(without alignments)
66.680 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 161 seqs, 1667 residues

Total number of hits satisfying chosen parameters: 322

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 162 summaries

Database : rni.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.8	74.0	19	1	US-08-846-020A-22	Sequence 22, Appl
	2	14.8	74.0	19	1	US-09-617-871-22	Sequence 22, Appl
c	3	12.2	61.0	17	1	US-09-866-108A-7612	Sequence 7612, Ap
	4	10.8	54.0	15	1	US-09-081-646-513	Sequence 513, App
	5	9.4	47.0	13	1	US-09-374-704-12	Sequence 12, Appl
c	6	9.4	47.0	13	1	US-09-374-704-13	Sequence 13, Appl
c	7	9	45.0	11	1	US-09-249-155A-122	Sequence 122, App
c	8	9	45.0	12	1	US-08-441-887A-200	Sequence 200, App
	9	8.4	42.0	10	1	US-08-202-927-31	Sequence 31, Appl
	10	8.4	42.0	10	1	US-08-202-927-35	Sequence 35, Appl
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c	12	8.4	42.0	10	1	US-08-488-551B-523	Sequence 523, App
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	15	8.4	42.0	10	1	US-09-908-510A-29	Sequence 29, Appl
	16	8.4	42.0	10	1	US-09-905-744B-29	Sequence 29, Appl
	17	8.4	42.0	10	1	US-10-107-660-29	Sequence 29, Appl
	18	8.4	42.0	10	1	US-10-107-576-29	Sequence 29, Appl
	19	8.4	42.0	10	1	US-09-905-732B-29	Sequence 29, Appl
	20	8.4	42.0	10	1	US-09-905-743B-29	Sequence 29, Appl
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	22	8.4	42.0	10	1	US-10-108-171A-29	Sequence 29, Appl
	23	8.4	42.0	10	1	PCT-US95-02419-31	Sequence 31, Appl
	24	8.4	42.0	10	1	PCT-US95-02419-35	Sequence 35, Appl
c	25	8.4	42.0	12	1	US-08-030-335-10	Sequence 10, Appl
c	26	8.4	42.0	12	1	US-07-973-431B-3	Sequence 3, Appli
c	27	8.4	42.0	12	1	US-08-122-433-26	Sequence 26, Appl
c	28	8.4	42.0	12	1	US-08-623-891-24	Sequence 24, Appl
c	29	8.4	42.0	12	1	US-08-480-020B-10	Sequence 10, Appl
c	30	8.4	42.0	12	1	US-08-910-618-10	Sequence 10, Appl
c	31	8.4	42.0	12	1	US-09-105-515-2	Sequence 2, Appli
c	32	8.4	42.0	12	1	US-08-910-322-10	Sequence 10, Appl
c	33	8.4	42.0	12	1	US-08-679-493A-68	Sequence 68, Appl
c	34	8.4	42.0	12	1	US-08-484-939A-10	Sequence 10, Appl
c	35	8.4	42.0	12	1	US-09-340-861-24	Sequence 24, Appl
c	36	8.4	42.0	12	1	US-09-634-262-24	Sequence 24, Appl
c	37	8.4	42.0	12	1	US-09-748-044-2	Sequence 2, Appli
c	38	8.4	42.0	12	1	US-09-384-472-10	Sequence 10, Appl
	39	8.4	42.0	12	1	US-09-835-370-54	Sequence 54, Appl
	40	8.4	42.0	12	1	US-09-793-146-38	Sequence 38, Appl
	41	8.4	42.0	12	1	US-09-793-146-48	Sequence 48, Appl
c	42	8.4	42.0	12	1	US-09-793-146-49	Sequence 49, Appl
	43	8	40.0	8	1	US-08-859-954-386	Sequence 386, App
	44	8	40.0	8	1	US-09-270-437D-22	Sequence 22, Appl
	45	8	40.0	8	1	5395759-14	Patent No. 5395759
	46	8	40.0	10	1	US-08-335-565A-17	Sequence 17, Appl
c	47	8	40.0	10	1	US-08-590-571-22	Sequence 22, Appl
	48	8	40.0	10	1	US-08-388-353-516	Sequence 516, App
	49	8	40.0	10	1	US-08-388-353-517	Sequence 517, App
	50	8	40.0	10	1	US-08-388-353-518	Sequence 518, App
	51	8	40.0	10	1	US-08-488-551B-516	Sequence 516, App
	52	8	40.0	10	1	US-08-488-551B-517	Sequence 517, App
	53	8	40.0	10	1	US-08-488-551B-518	Sequence 518, App
	54	8	40.0	10	1	US-08-488-551B-834	Sequence 834, App
	55	8	40.0	10	1	US-08-488-551B-835	Sequence 835, App
	56	8	40.0	10	1	US-08-488-551B-836	Sequence 836, App
c	57	8	40.0	10	1	US-08-906-691-12	Sequence 12, Appl
	58	8	40.0	10	1	US-09-508-753B-206	Sequence 206, App
	59	8	40.0	11	1	US-09-954-225-20	Sequence 20, Appl
	60	7.8	39.0	11	1	US-08-202-927-4	Sequence 4, Appli
	61	7.8	39.0	11	1	US-09-249-155A-61	Sequence 61, Appl
	62	7.8	39.0	11	1	US-09-249-155A-203	Sequence 203, App
c	63	7.8	39.0	11	1	US-09-351-657A-54	Sequence 54, Appl
	64	7.8	39.0	11	1	US-09-657-013-98	Sequence 98, Appl
	65	7.8	39.0	11	1	PCT-US95-02419-4	Sequence 4, Appli
	66	7.4	37.0	9	1	US-08-486-343A-7	Sequence 7, Appli
c	67	7.4	37.0	9	1	US-10-096-596-24	Sequence 24, Appl
c	68	7.4	37.0	9	1	US-09-990-186-2495	Sequence 2495, Ap
c	69	7.4	37.0	9	1	US-09-990-186-2496	Sequence 2496, Ap
	70	7.4	37.0	9	1	PCT-US95-07349-7	Sequence 7, Appli
c	71	7.4	37.0	10	1	US-07-651-710A-39	Sequence 39, Appl
c	72	7.4	37.0	10	1	US-08-486-955A-3	Sequence 3, Appli
c	73	7.4	37.0	10	1	US-08-477-396A-16	Sequence 16, Appl
c	74	7.4	37.0	10	1	US-08-388-353-522	Sequence 522, App
c	75	7.4	37.0	10	1	US-08-388-353-524	Sequence 524, App
c	76	7.4	37.0	10	1	US-08-488-551B-522	Sequence 522, App
c	77	7.4	37.0	10	1	US-08-488-551B-524	Sequence 524, App
c	78	7.4	37.0	10	1	US-08-488-551B-840	Sequence 840, App
c	79	7.4	37.0	10	1	US-09-075-215A-10	Sequence 10, Appl
c	80	7.4	37.0	10	1	US-09-154-750A-6	Sequence 6, Appli
c	81	7.4	37.0	10	1	US-07-868-539C-9	Sequence 9, Appli
	82	7.4	37.0	10	1	US-09-508-753B-34	Sequence 34, Appl
	83	7.4	37.0	10	1	US-09-508-753B-118	Sequence 118, App
c	84	7.4	37.0	10	1	US-09-508-753B-209	Sequence 209, App
	85	7.4	37.0	10	1	US-09-772-315-16	Sequence 16, Appl
c	86	7.4	37.0	10	1	US-09-377-497-53	Sequence 53, Appl
c	87	7.4	37.0	10	1	US-09-822-250A-22	Sequence 22, Appl
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	91	7.4	37.0	10	1	US-09-748-710-20	Sequence 20, Appl
c	92	7.4	37.0	10	1	US-09-821-694A-26	Sequence 26, Appl
	93	7.4	37.0	10	1	US-09-821-694A-30	Sequence 30, Appl
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	95	7	35.0	8	1	US-08-859-954-5	Sequence 5, Appli
	96	7	35.0	8	1	US-08-859-954-18	Sequence 18, Appl
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c	98	7	35.0	8	1	US-08-859-954-561	Sequence 561, App
c	99	7	35.0	9	1	US-09-159-274-31	Sequence 31, Appl
c	100	7	35.0	9	1	US-08-290-736C-12	Sequence 12, Appl
c	101	7	35.0	9	1	US-09-479-005A-1198	Sequence 1198, Ap
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	104	7	35.0	9	1	US-09-990-186-2103	Sequence 2103, Ap
	105	7	35.0	10	1	US-07-874-334-2	Sequence 2, Appli
	106	7	35.0	10	1	US-08-174-672D-113	Sequence 113, App

107	7	35.0	10	1	US-08-465-794-12	Sequence 12, Appl
c 108	7	35.0	10	1	US-08-822-701-5	Sequence 5, Appli
c 109	7	35.0	10	1	US-08-469-461-7	Sequence 7, Appli
c 110	7	35.0	10	1	US-08-724-354D-12	Sequence 12, Appl
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112	7	35.0	10	1	US-08-388-353-115	Sequence 115, App
113	7	35.0	10	1	US-08-388-353-116	Sequence 116, App
114	7	35.0	10	1	US-08-388-353-117	Sequence 117, App
115	7	35.0	10	1	US-08-388-353-118	Sequence 118, App
116	7	35.0	10	1	US-08-388-353-515	Sequence 515, App
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128	7	35.0	10	1	US-08-872-417B-4	Sequence 4, Appli
c 129	7	35.0	10	1	US-08-935-855-5	Sequence 5, Appli
c 130	7	35.0	10	1	US-09-063-450-32	Sequence 32, Appl
131	7	35.0	10	1	US-08-729-601A-67	Sequence 67, Appl
132	7	35.0	10	1	US-08-988-321B-29	Sequence 29, Appl
133	7	35.0	10	1	US-08-663-191A-5	Sequence 5, Appli
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135	7	35.0	10	1	US-09-436-518-4	Sequence 4, Appli
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c 139	7	35.0	10	1	US-09-598-326-100	Sequence 100, App
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153	7	35.0	10	1	US-08-935-377-17	Sequence 17, Appl
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155	7	35.0	10	1	US-09-910-469-76	Sequence 76, Appl
c 156	7	35.0	10	1	US-08-252-778-46	Sequence 46, Appl
157	7	35.0	10	1	US-09-977-615B-54	Sequence 54, Appl
158	7	35.0	10	1	US-10-111-708-6	Sequence 6, Appli
159	7	35.0	10	1	US-09-853-409-29	Sequence 29, Appl
c 160	7	35.0	10	1	US-09-030-832-23	Sequence 23, Appl
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c 162	6.4	32.0	10	1	5256545-14	Patent No. 5256545

ALIGNMENTS

```
RESULT 1
US-08-846-020A-22
; Sequence 22, Application US/08846020A
; Patent No. 6090547
; GENERAL INFORMATION:
;    APPLICANT:  Drazen M.D., Jeffrey M.
;    APPLICANT:  In M.D., Kwang-Ho
;    APPLICANT:  Asano M.D., Koichiro
;    APPLICANT:  Beier, David
;    APPLICANT:  Grobholz, James
;    TITLE OF INVENTION:  5-Lipoxygenase Gene Sequence
;    TITLE OF INVENTION:  Polymorphisms and Their Use in Classifying Patients
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHOATE, HALL & STEWART
;      STREET:  53 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2891
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,020A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jarrell Ph.D., Brenda H.
;      REGISTRATION NUMBER:  39,223
;      REFERENCE/DOCKET NUMBER:  0092662-0012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
;      TELEFAX:  (617) 248 4000
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
;    IMMEDIATE SOURCE:
;      CLONE:  Exon 4 sense primer
US-08-846-020A-22

  Query Match             74.0%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 4.2;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACATGGATG 19
              |||||| ||| |||||||
Db          2 CTCATGCTCAGATGGATG 19


RESULT 2
US-09-617-871-22
; Sequence 22, Application US/09617871
; Patent No. 6355434
; GENERAL INFORMATION:
;    APPLICANT:  Drazen M.D., Jeffrey M.
;    APPLICANT:  In M.D., Kwang-Ho
;    APPLICANT:  Asano M.D., Koichiro
;    APPLICANT:  Beier, David
;    APPLICANT:  Grobholz, James
;    TITLE OF INVENTION:  5-Lipoxygenase Gene Sequence
;    TITLE OF INVENTION:  Polymorphisms and Their Use in Classifying Patients
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHOATE, HALL & STEWART
;      STREET:  53 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2891
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/617,871
;      FILING DATE:
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/846,020
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jarrell Ph.D., Brenda H.
;      REGISTRATION NUMBER:  39,223
;      REFERENCE/DOCKET NUMBER:  0092662-0012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
;      TELEFAX:  (617) 248 4000
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
;    IMMEDIATE SOURCE:
;      CLONE:  Exon 4 sense primer
US-09-617-871-22

  Query Match           74.0%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 4.2;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACATGGATG 19
              |||||| ||| |||||||
Db          2 CTCATGCTCAGATGGATG 19


RESULT 3
US-09-866-108A-7612/c
; Sequence 7612, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7612
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-7612

  Query Match           61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 4
US-09-081-646-513
; Sequence 513, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Zhang, Lin
;  APPLICANT: Zhou, Wei
;  TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
;  TITLE OF INVENTION: Cancer Cells
;  FILE REFERENCE: 01107.74664
;  CURRENT APPLICATION NUMBER: US/09/081,646
;  CURRENT FILING DATE: 1998-05-20
;  EARLIER APPLICATION NUMBER: 60/047,352
;  EARLIER FILING DATE: 1997-05-21
;  NUMBER OF SEQ ID NOS: 871
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 513
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-081-646-513

  Query Match           54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 20;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              ||||| ||| ||||
Db          1 CATGGCCACGTGGA 14


RESULT 5
US-09-374-704-12
; Sequence 12, Application US/09374704
; Patent No. 6958240
; GENERAL INFORMATION:
;  APPLICANT: DERVAN, PETER B.
;  APPLICANT: BAIRD, ELDON J.
;  TITLE OF INVENTION: INHIBITION OF MAJOR GROOVE DNA BINDING
;  TITLE OF INVENTION: PROTEINS BY MODIFIED POLYAMIDES
;  FILE REFERENCE: 238/298
;  CURRENT APPLICATION NUMBER: US/09/374,704
;  CURRENT FILING DATE: 1999-08-12
;  EARLIER APPLICATION NUMBER: PCT/US98/02684
;  EARLIER FILING DATE: 1998-02-13
;  EARLIER APPLICATION NUMBER: PCT/US97/03332
;  EARLIER FILING DATE: 1997-02-20
;  EARLIER APPLICATION NUMBER: PCT/US97/12722
;  EARLIER FILING DATE: 1997-07-21
;  EARLIER APPLICATION NUMBER: 60/038,384
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 60/023,309
;  EARLIER FILING DATE: 1996-07-31
;  EARLIER APPLICATION NUMBER: 60/024,374
;  EARLIER FILING DATE: 1996-08-01
;  EARLIER APPLICATION NUMBER: 60/026,713
;  EARLIER FILING DATE: 1996-09-25
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;  EARLIER APPLICATION NUMBER: 08/853,522
;  EARLIER FILING DATE: 1997-05-08
;  EARLIER APPLICATION NUMBER: 08/837,524
;  EARLIER FILING DATE: 1997-04-21
;  EARLIER APPLICATION NUMBER: 08/607,078
;  EARLIER FILING DATE: 1996-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Polyamide Motif
US-09-374-704-12

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 29;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db          3 TCATGGTCATA 13


RESULT 6
US-09-374-704-13/c
; Sequence 13, Application US/09374704
; Patent No. 6958240
; GENERAL INFORMATION:
;  APPLICANT: DERVAN, PETER B.
;  APPLICANT: BAIRD, ELDON J.
;  TITLE OF INVENTION: INHIBITION OF MAJOR GROOVE DNA BINDING
;  TITLE OF INVENTION: PROTEINS BY MODIFIED POLYAMIDES
;  FILE REFERENCE: 238/298
;  CURRENT APPLICATION NUMBER: US/09/374,704
;  CURRENT FILING DATE: 1999-08-12
;  EARLIER APPLICATION NUMBER: PCT/US98/02684
;  EARLIER FILING DATE: 1998-02-13
;  EARLIER APPLICATION NUMBER: PCT/US97/03332
;  EARLIER FILING DATE: 1997-02-20
;  EARLIER APPLICATION NUMBER: PCT/US97/12722
;  EARLIER FILING DATE: 1997-07-21
;  EARLIER APPLICATION NUMBER: 60/038,384
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 60/023,309
;  EARLIER FILING DATE: 1996-07-31
;  EARLIER APPLICATION NUMBER: 60/024,374
;  EARLIER FILING DATE: 1996-08-01
;  EARLIER APPLICATION NUMBER: 60/026,713
;  EARLIER FILING DATE: 1996-09-25
;  EARLIER APPLICATION NUMBER: 08/853,522
;  EARLIER FILING DATE: 1997-05-08
;  EARLIER APPLICATION NUMBER: 08/837,524
;  EARLIER FILING DATE: 1997-04-21
;  EARLIER APPLICATION NUMBER: 08/607,078
;  EARLIER FILING DATE: 1996-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: GCN4 binding molecule
US-09-374-704-13

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 29;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db          3 TCATGGTCATA 13


RESULT 7
US-09-249-155A-122/c
; Sequence 122, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
;  APPLICANT:  Heber-Katz, Ellen
;  TITLE OF INVENTION:  Compositions and Methods for Wound
;  TITLE OF INVENTION:  Healing
;  FILE REFERENCE:  00486.78503
;  CURRENT APPLICATION NUMBER: US/09/249,155A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER:  US 60/074,737
;  PRIOR FILING DATE:  1998-02-13
;  PRIOR APPLICATION NUMBER:  US 60/097,937
;  PRIOR FILING DATE:  1998-08-26
;  PRIOR APPLICATION NUMBER:  US 60/102,051
;  PRIOR FILING DATE:  1998-09-28
;  NUMBER OF SEQ ID NOS:  346
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 122
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-249-155A-122

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGGTCACAT 14
              |||||||||
Db         10 TGGTCACAT 2


RESULT 8
US-08-441-887A-200/c
; Sequence 200, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;    APPLICANT:  Chee, Mark
;    APPLICANT:  Cronin, Maureen T.
;    APPLICANT:  Fodor, Stephen P.A.
;    APPLICANT:  Huang, Xiaohua X.
;    APPLICANT:  Hubbell, Earl A.
;    APPLICANT:  Lipshutz, Robert J.
;    APPLICANT:  Lobban, Peter E.
;    APPLICANT:  Morris, Macdonald S.
;    APPLICANT:  Sheldon, Edward L.
;    TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;    TITLE OF INVENTION:  Biological Chips
;    NUMBER OF SEQUENCES:  360
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,887A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/143,312
;      FILING DATE:  26-OCT-1993
```

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;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/082,937
;      FILING DATE:  25-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  018547-004160US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-326-2400
;      TELEFAX:  650-326-2422
;  INFORMATION FOR SEQ ID NO:  200:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (probe)
US-08-441-887A-200

  Query Match           45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 29;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
               |||||||||
Db         11 CATGGATGA 3


RESULT 9
US-08-202-927-31
; Sequence 31, Application US/08202927
; Patent No. 5646126
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Yung-chi
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Meyer Jr., Rich B.
;    APPLICANT:  Pai, Balakrishna S.
;    APPLICANT:  Reed, Michael W.
;    APPLICANT:  Zhou, James H.
;    TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
;    TITLE OF INVENTION:  Anticancer Activity
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klein & Szekeres
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,927
;      FILING DATE:  28-FEB-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  10
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "Nucleotide 10 has a tail which comprises
;      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
;      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
;      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
;      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
;      OTHER INFORMATION:  formula 3)."
US-08-202-927-31

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              ||||||| ||
Db          1 CACATGGGTG 10


RESULT 10
US-08-202-927-35
; Sequence 35, Application US/08202927
; Patent No. 5646126
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Yung-chi
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Meyer Jr., Rich B.
;    APPLICANT:  Pai, Balakrishna S.
;    APPLICANT:  Reed, Michael W.
;    APPLICANT:  Zhou, James H.
;    TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
;    TITLE OF INVENTION:  Anticancer Activity
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klein & Szekeres
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,927
;      FILING DATE:  28-FEB-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  10
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "Nucleotide 10 has a tail which comprises
;      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
;      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
;      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
;      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
;      OTHER INFORMATION:  formula 3)."
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```
US-08-202-927-35

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              |||| |||||
Db          1 CACACGGATG 10


RESULT 11
US-08-388-353-523/c
; Sequence 523, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  523:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-523

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         10 CTCAGGGTCA 1


RESULT 12
US-08-488-551B-523/c
; Sequence 523, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  523:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-523

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         10 CTCAGGGTCA 1


RESULT 13
US-08-488-551B-841/c
; Sequence 841, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/488,551B
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PM3864 (AU)
;       FILING DATE:  14-FEB-1994
;       APPLICATION NUMBER:  PM4002 (AU)
;       FILING DATE:  21-FEB-1994
;       APPLICATION NUMBER:  PN0284 (AU)
;       FILING DATE:  23-DEC-1994
;       APPLICATION NUMBER:  US 08/388,353
;       FILING DATE:  14-FEB-1995
;       APPLICATION NUMBER:  PN3021/95
;       FILING DATE:  17-MAY-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FRANK S. DIGIGLIO
;       REFERENCE/DOCKET NUMBER:  9606Z
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (516) 742-4343
;       TELEFAX:  (516) 742-4366
;   INFORMATION FOR SEQ ID NO:  841:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
US-08-488-551B-841

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         10 CTCAGGGTCA 1


RESULT 14
US-09-240-639-29
; Sequence 29, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT: Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/09/240,639
;  CURRENT FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-240-639-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 15
US-09-908-510A-29
; Sequence 29, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna Maria
;  TITLE OF INVENTION: METHODS AND  COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND N
;  TITLE OF INVENTION:  ACIDS
;  FILE REFERENCE: 28110/36120E
;  CURRENT APPLICATION NUMBER: US/09/908,510A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-908-510A-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 16
US-09-905-744B-29
; Sequence 29, Application US/09905744B
; Patent No. 6780410
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna Maria
;  TITLE OF INVENTION: METHODS AND  COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND N
;  TITLE OF INVENTION:  ACIDS
;  FILE REFERENCE: 28110/36120A
;  CURRENT APPLICATION NUMBER: US/09/905,744B
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-905-744B-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 17
US-10-107-660-29
; Sequence 29, Application US/10107660
; Patent No. 6780977
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/10/107,660
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: US/09/240,639
;  PRIOR FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-107-660-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 18
US-10-107-576-29
; Sequence 29, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna Maria
;  TITLE OF INVENTION: METHODS AND  COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
;  TITLE OF INVENTION:  ACIDS
;  FILE REFERENCE: 28110/36120H
;  CURRENT APPLICATION NUMBER: US/10/107,576
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-107-576-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 19
US-09-905-732B-29
; Sequence 29, Application US/09905732B
; Patent No. 6787328
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna Maria
;  TITLE OF INVENTION: METHODS AND  COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
;  FILE REFERENCE: 28110/36120B
;  CURRENT APPLICATION NUMBER: US/09/905,732B
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-905-732B-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 20
US-09-905-743B-29
; Sequence 29, Application US/09905743B
; Patent No. 6828423
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna Maria
;  TITLE OF INVENTION: METHODS AND  COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
;  TITLE OF INVENTION:  ACIDS
;  FILE REFERENCE: 28110/36120C
;  CURRENT APPLICATION NUMBER: US/09/905,743B
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-905-743B-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 21
US-09-905-589-29
; Sequence 29, Application US/09905589
; Patent No. 6884872
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/09/905,589
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: US/09/240,639
;  PRIOR FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-905-589-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 22
US-10-108-171A-29
; Sequence 29, Application US/10108171A
; Patent No. 6899875
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna Maria
;  TITLE OF INVENTION: METHODS AND  COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
```

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;  TITLE OF INVENTION:  ACIDS
;  FILE REFERENCE: 28110/36120F
;  CURRENT APPLICATION NUMBER: US/10/108,171A
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-108-171A-29

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 23
PCT-US95-02419-31
; Sequence 31, Application PC/TUS9502419
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Yung-chi
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Meyer Jr., Rich B.
;    APPLICANT:  Pai, Balakrishna S.
;    APPLICANT:  Reed, Michael W.
;    APPLICANT:  Zhou, James H.
;    TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
;    TITLE OF INVENTION:  Anticancer Activity
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klein & Szekeres
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02419
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/202,927
;      FILING DATE:  28-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  10
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "Nucleotide 10 has a tail which comprises
;      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
;      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
;      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
;      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
;      OTHER INFORMATION:  formula 3)."
PCT-US95-02419-31

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              ||||||| ||
Db          1 CACATGGGTG 10


RESULT 24
PCT-US95-02419-35
; Sequence 35, Application PC/TUS9502419
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Yung-chi
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Meyer Jr., Rich B.
;    APPLICANT:  Pai, Balakrishna S.
;    APPLICANT:  Reed, Michael W.
;    APPLICANT:  Zhou, James H.
;    TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
;    TITLE OF INVENTION:  Anticancer Activity
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klein & Szekeres
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02419
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/202,927
;      FILING DATE:  28-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  10
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "Nucleotide 10 has a tail which comprises
;      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
;      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
;      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
;      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
;      OTHER INFORMATION:  formula 3)."
PCT-US95-02419-35
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```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              |||| |||||
Db          1 CACACGGATG 10


RESULT 25
US-08-030-335-10/c
; Sequence 10, Application US/08030335
; Patent No. 5491073
;  GENERAL INFORMATION:
;    APPLICANT:  No. 5491073eborn, Matheus H
;    APPLICANT:  De Boer, Gerben F
;    TITLE OF INVENTION:  Cloning Of Chicken Anaemia DNA
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York, New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,335
;      FILING DATE:  08-MAR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Moran, Thomas F
;      REGISTRATION NUMBER:  16,579
;      REFERENCE/DOCKET NUMBER:  43276
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)-977-9550
;      TELEFAX:  (212)-977-9809
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-030-335-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 26
US-07-973-431B-3/c
; Sequence 3, Application US/07973431B
; Patent No. 5652144
;  GENERAL INFORMATION:
;    APPLICANT:  Lu, Yinchen
;    APPLICANT:  Haseltine, William A
;    TITLE OF INVENTION:  YC1 Protein, Gene, And Uses Thereof
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David G. Conlin; Dike, Bronstein,
;      ADDRESSEE:  Roberts & Cushman
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/973,431B
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eisenstein, Ronald I
;      REGISTRATION NUMBER:  30628
;      REFERENCE/DOCKET NUMBER:  41968
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
US-07-973-431B-3

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 27
US-08-122-433-26/c
; Sequence 26, Application US/08122433
; Patent No. 5683985
;  GENERAL INFORMATION:
;    APPLICANT:  Chu, Barbara C.F.
;    APPLICANT:  Orgel, Leslie
;    TITLE OF INVENTION:  OLIGODEOXYNUCLEOTIDES AND
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH
;    TITLE OF INVENTION:  SELECTIVELY BIND TO DEFINED DNA SEQUENCES
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/122,433
;      FILING DATE:  22-SEP-1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/687,337
;      FILING DATE:  18-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P31 9308
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  619-546-1995
;      TELEFAX:  619-546-9392
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-122-433-26

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 28
US-08-623-891-24/c
; Sequence 24, Application US/08623891
; Patent No. 5795778
;  GENERAL INFORMATION:
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HERPES SIMPLEX
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/623,891
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/238,200
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/987,133
;      FILING DATE:
;      APPLICATION NUMBER:  07/882,921
;      FILING DATE:  May 14, 1992
;      APPLICATION NUMBER:  07/948,359
;      FILING DATE:  September 18, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  200/209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-623-891-24

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 29
US-08-480-020B-10/c
; Sequence 10, Application US/08480020B
; Patent No. 5932476
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,020B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KUNG, VIOLA
;      REGISTRATION NUMBER:  P41,131
;      REFERENCE/DOCKET NUMBER:  VEOC.002.02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-480-020B-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 30
US-08-910-618-10/c
; Sequence 10, Application US/08910618
; Patent No. 5958424
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
```

```
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,618
;      FILING DATE:  13-AUG-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/484,939
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-910-618-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 31
US-09-105-515-2/c
; Sequence 2, Application US/09105515
; Patent No. 6113913
;  GENERAL INFORMATION:
;    APPLICANT:  BROUGH, DOUGLAS E.
;    TITLE OF INVENTION:  RECOMBINANT ADENOVIRUS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LEYDIG, VOIT & MAYER, LTD.
;      STREET:  TWO PRUDENTIAL PLAZA, SUITE 4900
;      CITY:  CHICAGO
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,515
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KILYK JR., JOHN
;      REGISTRATION NUMBER:  30763
;      REFERENCE/DOCKET NUMBER:  83827
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-09-105-515-2

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 32
US-08-910-322-10/c
; Sequence 10, Application US/08910322
; Patent No. 6238669
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,322
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/484,939
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-910-322-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 33
US-08-679-493A-68/c
; Sequence 68, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Ethan W.
;  TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
;  FILE REFERENCE: 55-95
;  CURRENT APPLICATION NUMBER: US/08/679,493A
;  CURRENT FILING DATE:  1996-07-12
;  PRIOR APPLICATION NUMBER: 60/001203
;  PRIOR FILING DATE: 1995-07-14
;  PRIOR APPLICATION NUMBER: 60/003,112
;  PRIOR FILING DATE: 1995-09-01
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
;   LENGTH: 12
;   TYPE: RNA
;   ORGANISM: Human immunodeficiency virus type 1
US-08-679-493A-68

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         11 CTCAGGGTCA 2


RESULT 34
US-08-484-939A-10/c
; Sequence 10, Application US/08484939A
; Patent No. 6319693
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,939A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-484-939A-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 35
US-09-340-861-24/c
; Sequence 24, Application US/09340861
; Patent No. 6432704
;  GENERAL INFORMATION:
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HERPES SIMPLEX
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/340,861
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/987,133
;      FILING DATE:
;      APPLICATION NUMBER:  07/882,921
;      FILING DATE:  May 14, 1992
;      APPLICATION NUMBER:  07/948,359
;      FILING DATE:  September 18, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  200/209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
```

```
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-340-861-24

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 36
US-09-634-262-24/c
; Sequence 24, Application US/09634262
; Patent No. 6440719
;  GENERAL INFORMATION:
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HERPES SIMPLEX
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/634,262
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/987,133
;      FILING DATE:
;      APPLICATION NUMBER:  07/882,921
;      FILING DATE:  May 14, 1992
;      APPLICATION NUMBER:  07/948,359
;      FILING DATE:  September 18, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  200/209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-634-262-24

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 37
US-09-748-044-2/c
; Sequence 2, Application US/09748044
; Patent No. 6458578
; GENERAL INFORMATION:
;  APPLICANT: Brough, Douglas E.
;  APPLICANT:  Kovesdi, Imre
;  TITLE OF INVENTION: Recombinant Cell Line
;  FILE REFERENCE: 207952
;  CURRENT APPLICATION NUMBER: US/09/748,044
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: PCT/US99/14333
;  PRIOR FILING DATE: 1999-06-24
;  PRIOR APPLICATION NUMBER: US 09/105,515
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Adenovirus type 5
US-09-748-044-2

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 38
US-09-384-472-10/c
; Sequence 10, Application US/09384472
; Patent No. 6509446
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/384,472
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,939
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
```

```
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-384-472-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 39
US-09-835-370-54
; Sequence 54, Application US/09835370
; Patent No. 6777544
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  APPLICANT:  WILL, DAVID W
;  TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
;  TITLE OF INVENTION:  PROCESSES FOR PREPARING THEM
;  FILE REFERENCE: 02481.1742 SEQUENCE LISTING
;  CURRENT APPLICATION NUMBER: US/09/835,370
;  CURRENT FILING DATE:  2001-04-17
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  nucleotide
;   OTHER INFORMATION: base sequence of PNA derivatives that bind to
;   OTHER INFORMATION: viral and cellular targets
US-09-835-370-54

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 40
US-09-793-146-38
; Sequence 38, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/09/793,146
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-38

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 41
US-09-793-146-48
; Sequence 48, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/09/793,146
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-48

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 42
US-09-793-146-49/c
; Sequence 49, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/09/793,146
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
```

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;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-49

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity  90.0%;  Pred. No. 40;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db         11 CATCATGGTC 2


RESULT 43
US-08-859-954-386
; Sequence 386, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  386:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-386

  Query Match           40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 ATGGTCAC 12
              ||||||||
Db          1 ATGGTCAC 8


RESULT 44
US-09-270-437D-22
; Sequence 22, Application US/09270437D
; Patent No. 6830924
; GENERAL INFORMATION:
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT:  Gure, Ali
;  APPLICANT:  Tsang, Solam
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Jager, Elke
;  APPLICANT:  Knuth, Alexander
;  APPLICANT:  Old, Lloyd J.
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antiger
;  TITLE OF INVENTION:  Antigens Per Se, And Uses Thereof
;  FILE REFERENCE: LUD 5538.1
;  CURRENT APPLICATION NUMBER: US/09/270,437D
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER: 09/061,709
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 22
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: adaptor
;   LOCATION: 1...8
;   OTHER INFORMATION: synthetic adaptor sequence
US-09-270-437D-22

  Query Match           40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              ||||||||
Db          1 CATGGATG 8


RESULT 45
5395759-14
;Patent No. 5395759
;    APPLICANT: HOLMES, IAN H.;DYALL-SMITH, MICHAEL L.
;    TITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCE
;ENCODING THE HUMAN ROTAVIRUS MAJOR OUTER CAPSID GLYCOPROTEIN
;    NUMBER OF SEQUENCES: 14
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/474,642
;      FILING DATE: 29-APR-1985
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 824,704
;      FILING DATE: 04-FEB-1987
;SEQ ID NO:14:
;      LENGTH: 8
5395759-14

  Query Match           40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACAT 14
              ||||||||
Db          1 GGTCACAT 8


RESULT 46
US-08-335-565A-17
; Sequence 17, Application US/08335565A
; Patent No. 5527671
;  GENERAL INFORMATION:
;    APPLICANT:  Li, Kening
;    APPLICANT:  Rouse, Douglas I.
```

```
;    APPLICANT:  German, Thomas L.
;    TITLE OF INVENTION:  ASSAY FOR VERTICILLIUM DAHLIAE
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles and Brady
;      STREET:  1 South Pinckney St., PO BOX 2113
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/335,565A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27,386
;      REFERENCE/DOCKET NUMBER:  960296.93065
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-335-565A-17

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           1 ATGGATGA 8


RESULT 47
US-08-590-571-22/c
; Sequence 22, Application US/08590571
; Patent No. 5861246
;  GENERAL INFORMATION:
;    APPLICANT:  Sherman Weissman and Girish N. Nallur
;    TITLE OF INVENTION:  MULTIPLE SELECTION PROCESS
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/590,571
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  Yale
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-590-571-22

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CATGGATG 19
               ||||||||
Db          10 CATGGATG 3


RESULT 48
US-08-388-353-516
; Sequence 516, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  516:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-516

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           3 ATGGATGA 10
```

```
RESULT 49
US-08-388-353-517
; Sequence 517, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  517:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-517

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           2 ATGGATGA 9


RESULT 50
US-08-388-353-518
; Sequence 518, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  518:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-518

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           1 ATGGATGA 8


RESULT 51
US-08-488-551B-516
; Sequence 516, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  516:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-516

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           3 ATGGATGA 10


RESULT 52
US-08-488-551B-517
; Sequence 517, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  517:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-517

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           2 ATGGATGA 9


RESULT 53
US-08-488-551B-518
; Sequence 518, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  518:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-518

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           1 ATGGATGA 8


RESULT 54
US-08-488-551B-834
; Sequence 834, Application US/08488551B
```

```
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  834:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-834

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          3 ATGGATGA 10


RESULT 55
US-08-488-551B-835
; Sequence 835, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  835:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-835

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 56
US-08-488-551B-836
; Sequence 836, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
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;       FILING DATE:  21-FEB-1994
;       APPLICATION NUMBER:  PN0284 (AU)
;       FILING DATE:  23-DEC-1994
;       APPLICATION NUMBER:  US 08/388,353
;       FILING DATE:  14-FEB-1995
;       APPLICATION NUMBER:  PN3021/95
;       FILING DATE:  17-MAY-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FRANK S. DIGIGLIO
;       REFERENCE/DOCKET NUMBER:  9606Z
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (516) 742-4343
;       TELEFAX:  (516) 742-4366
;   INFORMATION FOR SEQ ID NO:  836:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
US-08-488-551B-836

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
               ||||||||
Db          1 ATGGATGA 8


RESULT 57
US-08-906-691-12/c
; Sequence 12, Application US/08906691
; Patent No. 6066452
;  GENERAL INFORMATION:
;     APPLICANT:  Weissman, Sherman M.
;     APPLICANT:  Nallur, Girish N.
;     APPLICANT:  Kulkarni, Prakash
;     TITLE OF INVENTION:  MULTIPLEX SELECTION TECHNIQUE FOR
;     TITLE OF INVENTION:  IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS
;     NUMBER OF SEQUENCES:  50
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SEED and BERRY LLP
;       STREET:  6300 Columbia Center, 701 Fifth Avenu
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  USA
;       ZIP:  981094
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/906,691
;       FILING DATE:  31-JUL-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  No. 6066452tenburg Ph.D., Carol
;       REGISTRATION NUMBER:  39,317
;       REFERENCE/DOCKET NUMBER:  390036.403C1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
US-08-906-691-12

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
               ||||||||
Db         10 CATGGATG 3


RESULT 58
US-09-508-753B-206
; Sequence 206, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 206
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-206

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
               ||||||||
Db          3 TCATGGTC 10


RESULT 59
US-09-954-225-20
; Sequence 20, Application US/09954225
; Patent No. 6855498
; GENERAL INFORMATION:
;  APPLICANT: HESTER, JEFFREY D.
;  APPLICANT:  LINDQUIST, ALAN
;  APPLICANT:  SCHAEFER, FRANK W.
;  TITLE OF INVENTION: IN-SITU HYBRIDIZATION PROBES FOR THE DETECTION OF
;  TITLE OF INVENTION:  MICROSPORIDIAL SPECIES
;  FILE REFERENCE: EPA-C132
;  CURRENT APPLICATION NUMBER: US/09/954,225
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/234,241
;  PRIOR FILING DATE: 2000-09-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 11
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Species
;   OTHER INFORMATION: specific probe for No. 6855498ema furnacalis
US-09-954-225-20

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 40;
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  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCACATGG 16
              :||||:||
Db          3 UCACAUGG 10


RESULT 60
US-08-202-927-4
; Sequence 4, Application US/08202927
; Patent No. 5646126
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Yung-chi
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Meyer Jr., Rich B.
;    APPLICANT:  Pai, Balakrishna S.
;    APPLICANT:  Reed, Michael W.
;    APPLICANT:  Zhou, James H.
;    TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
;    TITLE OF INVENTION:  Anticancer Activity
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klein & Szekeres
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,927
;      FILING DATE:  28-FEB-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  11
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "Nucleotide 11 has a tail which comprises
;      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
;      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
;      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
;      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
;      OTHER INFORMATION:  formula 3)."
US-08-202-927-4

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CACATGGATGA 20
              |||| || |||
Db          1 CACACGGGTGA 11


RESULT 61
US-09-249-155A-61
; Sequence 61, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
;  APPLICANT:  Heber-Katz, Ellen
;  TITLE OF INVENTION:  Compositions and Methods for Wound
;  TITLE OF INVENTION:  Healing
;  FILE REFERENCE:  00486.78503
;  CURRENT APPLICATION NUMBER: US/09/249,155A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER:  US 60/074,737
;  PRIOR FILING DATE:  1998-02-13
;  PRIOR APPLICATION NUMBER:  US 60/097,937
;  PRIOR FILING DATE:  1998-08-26
;  PRIOR APPLICATION NUMBER:  US 60/102,051
;  PRIOR FILING DATE:  1998-09-28
;  NUMBER OF SEQ ID NOS:  346
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-249-155A-61

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||| ||| |||
Db          1 CTCCTGGACAC 11


RESULT 62
US-09-249-155A-203
; Sequence 203, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
;  APPLICANT:  Heber-Katz, Ellen
;  TITLE OF INVENTION:  Compositions and Methods for Wound
;  TITLE OF INVENTION:  Healing
;  FILE REFERENCE:  00486.78503
;  CURRENT APPLICATION NUMBER: US/09/249,155A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER:  US 60/074,737
;  PRIOR FILING DATE:  1998-02-13
;  PRIOR APPLICATION NUMBER:  US 60/097,937
;  PRIOR FILING DATE:  1998-08-26
;  PRIOR APPLICATION NUMBER:  US 60/102,051
;  PRIOR FILING DATE:  1998-09-28
;  NUMBER OF SEQ ID NOS:  346
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 203
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-249-155A-203

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||| ||| |||
Db          1 CTCCTGGACAC 11


RESULT 63
US-09-351-657A-54/c
; Sequence 54, Application US/09351657A
; Patent No. 6545140
; GENERAL INFORMATION:
;  APPLICANT: Harmon, Barry G.
;  APPLICANT:  Jackwood, Mark W.
```

```
;  APPLICANT:  Brockus, Charles W.
;  TITLE OF INVENTION: DNA encoding an avian beta-defensin and uses thereof
;  FILE REFERENCE: 757.007US1
;  CURRENT APPLICATION NUMBER: US/09/351,657A
;  CURRENT FILING DATE:  1999-07-13
;  PRIOR APPLICATION NUMBER: US 60/092,668
;  PRIOR FILING DATE: 1998-07-13
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
;   LENGTH: 11
;   TYPE: RNA
;   ORGANISM: Gallus gallus
US-09-351-657A-54

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              |||||| |||
Db         11 CATGGTTTCAT 1


RESULT 64
US-09-657-013-98
; Sequence 98, Application US/09657013
; Patent No. 6709817
; GENERAL INFORMATION:
;  APPLICANT: Zoghbi, Huda Y.
;  APPLICANT:  Van den Veyver, Ignatia B
;  APPLICANT:  Amir, Ruthie
;  APPLICANT:  Francke, Uta
;  TITLE OF INVENTION: Methods of Identifying Mutations in a Methyl-CPG-Binding Domain
;  TITLE OF INVENTION:  Containing Gene or Protein in Neurodevelopmental Disease and Tre
;  FILE REFERENCE: HO-P01893US1/09905371
;  CURRENT APPLICATION NUMBER: US/09/657,013
;  CURRENT FILING DATE:  2000-09-07
;  PRIOR APPLICATION NUMBER: US 60/152,778
;  PRIOR FILING DATE: 1999-09-07
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Human
US-09-657-013-98

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCA 11
              | ||||||| |
Db          1 CTTCATGGTAA 11


RESULT 65
PCT-US95-02419-4
; Sequence 4, Application PC/TUS9502419
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Yung-chi
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Meyer Jr., Rich B.
;    APPLICANT:  Pai, Balakrishna S.
;    APPLICANT:  Reed, Michael W.
;    APPLICANT:  Zhou, James H.
;    TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
;    TITLE OF INVENTION:  Anticancer Activity
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klein & Szekeres
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02419
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/202,927
;      FILING DATE:  28-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  11
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "Nucleotide 11 has a tail which comprises
;      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
;      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
;      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
;      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
;      OTHER INFORMATION:  formula 3)."
PCT-US95-02419-4

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CACATGGATGA 20
              |||| || |||
Db          1 CACACGGGTGA 11


RESULT 66
US-08-486-343A-7
; Sequence 7, Application US/08486343A
; Patent No. 6071695
;  GENERAL INFORMATION:
;    APPLICANT:  OZKAYNAK, ENGIN
;    APPLICANT:  OPPERMANN, HERMANN
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR MODULATING
;    TITLE OF INVENTION:  MORPHOGENIC PROTEIN EXPRESSION
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
;      ADDRESSEE:  INC.
;      STREET:  45 SOUTH STREET
;      CITY:  HOPKINTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  07148
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,343A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PITCHER, Edmund R
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-091CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)-248-7000
;      TELEFAX:  (617)-248-7100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..9
;      OTHER INFORMATION:  /note= "HUMAN FTZ BINDING SITE"
US-08-486-343A-7

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCA 11
              ||| |||||
Db          1 TCAAGGTCA 9


RESULT 67
US-10-096-596-24/c
; Sequence 24, Application US/10096596
; Patent No. 6746845
; GENERAL INFORMATION:
;  APPLICANT: Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  APPLICANT:  Velculescu, Victor
;  APPLICANT:  Zhang, Lin
;  TITLE OF INVENTION: METHOD FOR SERIAL ANLAYSIS OF GENE EXPRESSION
;  FILE REFERENCE: 001107.00242
;  CURRENT APPLICATION NUMBER: US/10/096,596
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: US 08/527,154
;  PRIOR FILING DATE: 1995-09-12
;  PRIOR APPLICATION NUMBER: US 08/544,861
;  PRIOR FILING DATE: 1995-10-18
;  PRIOR APPLICATION NUMBER: US 09/107,228
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-096-596-24

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 68
US-09-990-186-2495/c
; Sequence 2495, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2495
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2495

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGG 16
              |||||| ||
Db          9 GTCACACGG 1


RESULT 69
US-09-990-186-2496/c
; Sequence 2496, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2496
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2496

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGG 16
              |||||| ||
Db          9 GTCACACGG 1


RESULT 70
PCT-US95-07349-7
; Sequence 7, Application PC/TUS9507349
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR MODULATING
;    TITLE OF INVENTION:  MORPHOGEN EXPRESSION
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
;      ADDRESSEE:  INC.
;      STREET:  45 SOUTH STREET
;      CITY:  HOPKINTON
;      STATE:  MA
;      COUNTRY:  USA
```

```
;      ZIP:  07148
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07349
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/938,021
;      FILING DATE:  28-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KELLEY, ROBIN D
;      REGISTRATION NUMBER:  34,637
;      REFERENCE/DOCKET NUMBER:  CRP-091PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508)-435-9001
;      TELEFAX:  (508)-435-0992
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..9
;      OTHER INFORMATION:  /note= "HUMAN TFZ BINDING SITE"
PCT-US95-07349-7

  Query Match           37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCA 11
              ||| |||||
Db          1 TCAAGGTCA 9


RESULT 71
US-07-651-710A-39/c
; Sequence 39, Application US/07651710A
; Patent No. 5362864
;  GENERAL INFORMATION:
;    APPLICANT:  Chua, Nam-Hai
;    TITLE OF INVENTION:  Trans-Activating Factor-1
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/651,710A
;      FILING DATE:  19910206
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  3288-014
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  TAF-1 binding motif
US-07-651-710A-39

  Query Match           37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGG 16
              ||||| |||
Db         10 GTCACGTGG 2


RESULT 72
US-08-486-955A-3/c
; Sequence 3, Application US/08486955A
; Patent No. 5747299
;  GENERAL INFORMATION:
;    APPLICANT:  FATHMAN, Garrison
;    APPLICANT:  BLOOM, Debra
;    TITLE OF INVENTION:  Anergy Genes
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,955A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I.
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  A59741-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-486-955A-3

  Query Match           37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 73
US-08-477-396A-16/c
; Sequence 16, Application US/08477396A
; Patent No. 5872235
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Lan Bo
;    APPLICANT:  Bao, Shideng
;    APPLICANT:  Liu, Yuan
;    TITLE OF INVENTION:  A NOVEL TUMOR MARKER AND NOVEL METHOD OF
;    TITLE OF INVENTION:  ISOLATING SAME
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weingarten, Schurgin, Gagnebin & Hayes
;      STREET:  Ten Post Office Square
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,396A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/146,488
;      FILING DATE:  29-OCT-1993
;      APPLICATION NUMBER:  US 08/448,388
;      FILING DATE:  28-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/12502
;      FILING DATE:  31-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heine, Holliday C.
;      REGISTRATION NUMBER:  34,346
;      REFERENCE/DOCKET NUMBER:  DFCI-333BX
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-2290
;      TELEFAX:  (617) 451-0313
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-477-396A-16

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 74
US-08-388-353-522/c
; Sequence 522, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  522:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-522

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 TCATGGTCA 11
                ||| |||||
Db          10 TCAGGGTCA 2


RESULT 75
US-08-388-353-524/c
; Sequence 524, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
```

```
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  524:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-524

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              |||| ||||
Db          9 CTCAGGGTC 1


RESULT 76
US-08-488-551B-522/c
; Sequence 522, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  522:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-522

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCA 11
              ||| |||||
Db         10 TCAGGGTCA 2


RESULT 77
US-08-488-551B-524/c
; Sequence 524, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  524:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-524

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              |||| ||||
Db          9 CTCAGGGTC 1


RESULT 78
US-08-488-551B-840/c
; Sequence 840, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
```

```
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  840:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-840

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCA 11
              ||| |||||
Db         10 TCAGGGTCA 2


RESULT 79
US-09-075-215A-10/c
; Sequence 10, Application US/09075215A
; Patent No. 6054571
;  GENERAL INFORMATION:
;    APPLICANT:  JOLICOEUR, Paul
;    APPLICANT:  BALSALOBRE, Aurelio
;    TITLE OF INVENTION:  dft-A GENE, DIAGNOSTIC AND
;    TITLE OF INVENTION:  THERAPEUTIC USES THEREOF
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swabey Ogilvy Renault
;      STREET:  Suite 1600, 1981 McGill College
;      CITY:  Montreal
;      STATE:  QC
;      COUNTRY:  Canada
;      ZIP:  H3A 2Y3
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/075,215A
;      FILING DATE:  11-MAY-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ctt, France
;      REGISTRATION NUMBER:  37,037
;      REFERENCE/DOCKET NUMBER:  13497-4"US" FC/ld
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  514-845-7126
;      TELEFAX:  514-288-8389
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-075-215A-10

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 80
US-09-154-750A-6/c
; Sequence 6, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
;  APPLICANT: Vogelstein, Bert
;  APPLICANT:  Kinzler, Kenneth
;  APPLICANT:  Polyak, Kornelia
;  TITLE OF INVENTION: p53-Induced Apoptosis
;  FILE REFERENCE: 1107.75357
;  CURRENT APPLICATION NUMBER: US/09/154,750A
;  CURRENT FILING DATE:  1998-09-17
;  PRIOR APPLICATION NUMBER: 60/059,153
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/079817
;  PRIOR FILING DATE: 1998-03-30
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-154-750A-6

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 81
US-07-868-539C-9/c
; Sequence 9, Application US/07868539C
; Patent No. 6521601
```

```
; GENERAL INFORMATION:
;  APPLICANT: Carman, Mark
;  TITLE OF INVENTION: METHODS AND COMPOSITION FOR INHIBITION OF VIRAL REPLICATION
;  FILE REFERENCE: 10624-089-999
;  CURRENT APPLICATION NUMBER: US/07/868,539C
;  CURRENT FILING DATE:  1992-04-14
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: herpes simplex virus
US-07-868-539C-9

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATG 15
              |||||| ||
Db          9 GGTCACGTG 1


RESULT 82
US-09-508-753B-34
; Sequence 34, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 34
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-34

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATG 19
              ||| |||||
Db          2 ACAAGGATG 10


RESULT 83
US-09-508-753B-118
; Sequence 118, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 118
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-118

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              || ||||||
Db          2 CAAGGTCAC 10


RESULT 84
US-09-508-753B-209/c
; Sequence 209, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 209
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-209

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATG 19
              ||| |||||
Db          9 ACAAGGATG 1


RESULT 85
US-09-772-315-16
; Sequence 16, Application US/09772315
; Patent No. 6559125
; GENERAL INFORMATION:
;  APPLICANT: DERVAN, Peter
;  APPLICANT:  WURTZ, Nicholas
;  APPLICANT:  CHANG, Aileen
;  TITLE OF INVENTION: POLYAMIDE-ALKYLATOR CONJUGATES & RELATED PRODUCTS & METHODS
;  FILE REFERENCE: GENESOFT09/772315
;  CURRENT APPLICATION NUMBER: US/09/772,315
;  CURRENT FILING DATE:  2001-01-26
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Description of Artificial Sequence: Polyamide-Alkylator
;   OTHER INFORMATION: Conjugate Target Sequence
US-09-772-315-16

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACA 13
              ||||||| |
Db          1 ATGGTCATA 9


RESULT 86
US-09-377-497-53/c
; Sequence 53, Application US/09377497
; Patent No. 6670119
; GENERAL INFORMATION:
;  APPLICANT: YOSHIKAWA, YOSHIE
;  APPLICANT: MUKAI, HIROYUKI
;  APPLICANT: ASADA, KIYOZO
;  APPLICANT: HINO, FUMITSUGU
;  APPLICANT: KATO, IKUNOSHIN
;  TITLE OF INVENTION: CANCER-ASSOCIATED GENES
;  FILE REFERENCE: 1422-388P
;  CURRENT APPLICATION NUMBER: US/09/377,497
;  CURRENT FILING DATE: 1999-08-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: any n or Xaa = unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-377-497-53

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 87
US-09-822-250A-22/c
; Sequence 22, Application US/09822250A
; Patent No. 6706477
; GENERAL INFORMATION:
;  APPLICANT: Zauderer, Maurice
;  TITLE OF INVENTION: Methods for Producing Polynucleotide Libraries in Vaccinia Virus
;  FILE REFERENCE: 1821.0010001
;  CURRENT APPLICATION NUMBER: US/09/822,250A
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 08/935,377
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Ldd1 primer
US-09-822-250A-22

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 88
US-10-034-350A-22/c
; Sequence 22, Application US/10034350A
; Patent No. 6800442
; GENERAL INFORMATION:
;  APPLICANT: Zauderer, Maurice
;  TITLE OF INVENTION: Methods of Selecting Polynucleotides Encoding Antigens
;  FILE REFERENCE: 1821.0010002
;  CURRENT APPLICATION NUMBER: US/10/034,350A
;  CURRENT FILING DATE:  2002-01-03
;  PRIOR APPLICATION NUMBER: US 08/935,377
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-034-350A-22

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 89
US-08-935-377-22/c
; Sequence 22, Application US/08935377
; Patent No. 6872518
;  GENERAL INFORMATION:
;    APPLICANT:  Zauderer, Maurice
;    TITLE OF INVENTION:  T Cells Specific for Target Antigens and
;    TITLE OF INVENTION:  Vaccines Based Thereon
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,377
;      FILING DATE:  22-SEP-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1821.0010000/EKS/CMB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-935-377-22

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 90
US-09-748-710-16
; Sequence 16, Application US/09748710
; Patent No. 6916610
; GENERAL INFORMATION:
;  APPLICANT: WANG, SAN MING
;  APPLICANT:  CHEN, JIANJUN
;  APPLICANT:  ROWLEY, JANET D.
;  TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER cDNA FRAGMENTS
;  TITLE OF INVENTION:  FROM SAGE TAGS FOR GENE IDENTIFICATION
;  FILE REFERENCE: ARCD:343US
;  CURRENT APPLICATION NUMBER: US/09/748,710
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: 60/174,391
;  PRIOR FILING DATE: 2000-01-03
;  PRIOR APPLICATION NUMBER: 60/173,617
;  PRIOR FILING DATE: 1999-12-29
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-748-710-16

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              || ||||||
Db          1 CTTATGGTC 9


RESULT 91
US-09-748-710-20
; Sequence 20, Application US/09748710
; Patent No. 6916610
; GENERAL INFORMATION:
;  APPLICANT: WANG, SAN MING
;  APPLICANT:  CHEN, JIANJUN
;  APPLICANT:  ROWLEY, JANET D.
;  TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER cDNA FRAGMENTS
;  TITLE OF INVENTION:  FROM SAGE TAGS FOR GENE IDENTIFICATION
;  FILE REFERENCE: ARCD:343US
;  CURRENT APPLICATION NUMBER: US/09/748,710
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: 60/174,391
;  PRIOR FILING DATE: 2000-01-03
;  PRIOR APPLICATION NUMBER: 60/173,617
;  PRIOR FILING DATE: 1999-12-29
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-748-710-20

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              || ||||||
Db          1 CTTATGGTC 9


RESULT 92
US-09-821-694A-26/c
; Sequence 26, Application US/09821694A
; Patent No. 6949340
; GENERAL INFORMATION:
;  APPLICANT: HILLS, WILLIAM D.
;  TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
;  TITLE OF INVENTION:  HYBRIDIZATION
;  FILE REFERENCE: 0450-0001
;  CURRENT APPLICATION NUMBER: US/09/821,694A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Decoder
;   OTHER INFORMATION: binding sequence
US-09-821-694A-26

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATG 19
              | |||||||
Db         10 AGATGGATG 2


RESULT 93
US-09-821-694A-30
; Sequence 30, Application US/09821694A
; Patent No. 6949340
; GENERAL INFORMATION:
;  APPLICANT: HILLS, WILLIAM D.
;  TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
;  TITLE OF INVENTION:  HYBRIDIZATION
;  FILE REFERENCE: 0450-0001
;  CURRENT APPLICATION NUMBER: US/09/821,694A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Decoder probe
;   OTHER INFORMATION: sequence
US-09-821-694A-30

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          11 ACATGGATG 19
               | |||||||
Db           1 AGATGGATG 9


RESULT 94
5256545-14
;Patent No. 5256545
;     APPLICANT: BROWN, MICHAEL S.;GOLDSTEIN, JOSEPH L.;RUSSELL,
;DAVID W.;SUDHOF, THOMAS C.
;     TITLE OF INVENTION: STEROL REGULATORY ELEMENTS
;     NUMBER OF SEQUENCES: 42
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/425,852
;       FILING DATE: 20-OCT-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 33,330
;       FILING DATE: 30-MAR-1987
;       APPLICATION NUMBER: 33,081
;       FILING DATE: 30-MAR-1987
;SEQ ID NO:14:
;       LENGTH: 10
5256545-14

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               |||| ||||
Db           1 CATGCATGA 9


RESULT 95
US-08-859-954-5
; Sequence 5, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;     APPLICANT:  Hardin, Susan H.
;     APPLICANT:  Homayouni, Ramin
;     APPLICANT:  Hardin, Paul E.
;     TITLE OF INVENTION:  Design and Optimized Primer Library for
;     TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;     NUMBER OF SEQUENCES:  566
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fulbright & Jaworski L.L.P.
;       STREET:  1301 McKinney, Suite 5100
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  U.S.A.
;       ZIP:  77010-3095
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,954
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,782
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Paul, Thomas D.
;       REGISTRATION NUMBER:  32,714
;       REFERENCE/DOCKET NUMBER:  D-5900
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713/651-5325
;       TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  YES
US-08-859-954-5

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGT 9
               |||||||
Db          2 TCATGGT 8


RESULT 96
US-08-859-954-18
; Sequence 18, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;     APPLICANT:  Hardin, Susan H.
;     APPLICANT:  Homayouni, Ramin
;     APPLICANT:  Hardin, Paul E.
;     TITLE OF INVENTION:  Design and Optimized Primer Library for
;     TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;     NUMBER OF SEQUENCES:  566
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fulbright & Jaworski L.L.P.
;       STREET:  1301 McKinney, Suite 5100
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  U.S.A.
;       ZIP:  77010-3095
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,954
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,782
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Paul, Thomas D.
;       REGISTRATION NUMBER:  32,714
;       REFERENCE/DOCKET NUMBER:  D-5900
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713/651-5325
;       TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  YES
US-08-859-954-18

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACAT 14
```

```
                  |||||||
Db          1 GTCACAT 7


RESULT 97
US-08-859-954-366/c
; Sequence 366, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  366:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-366

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
                |||||||
Db          8 ATGGATG 2


RESULT 98
US-08-859-954-561/c
; Sequence 561, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  561:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-561

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGGATGA 20
                |||||||
Db          7 TGGATGA 1


RESULT 99
US-09-159-274-31/c
; Sequence 31, Application US/09159274
; Patent No. 6127173
; GENERAL INFORMATION:
;  APPLICANT: MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.
;  TITLE OF INVENTION: NUCLEIC ACID CATALYSTS WITH ENDONUCLEASE ACTIVITY
;  FILE REFERENCE: 236/200-US
;  CURRENT APPLICATION NUMBER: US/09/159,274
;  CURRENT FILING DATE: 1998-09-22
;  EARLIER APPLICATION NUMBER: US 60/059,473
;  EARLIER FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
;   LENGTH: 9
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthesized nucleic acid molecule
US-09-159-274-31

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CCTCATG 7
              |||||||
Db          8 CCTCATG 2


RESULT 100
US-08-290-736C-12/c
; Sequence 12, Application US/08290736C
; Patent No. 6294174
;   GENERAL INFORMATION:
;        APPLICANT: KRSMANOVIC, VELIBOR
;                   COSIC, IRENA
;                   BIQUARD, JEAN-MICHEL
;                   HEARN, MILTON TW
;        TITLE OF INVENTION: PEPTIDES IMMUNOLOGICALLY RELATED TO
;                            PROTEINS OF A VIRAL AGENT AND THEIR BIOLOGICAL APPLICATION
;        NUMBER OF SEQUENCES: 48
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/290,736C
;             FILING DATE: 16-No. 6294174-1994
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/FR93/00171
;             FILING DATE: 19-FEB-1993
;             APPLICATION NUMBER: FR92/01883
;             FILING DATE: 19-FEB-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B.J.
;             REGISTRATION NUMBER: 36663
;             REFERENCE/DOCKET NUMBER: 1721-3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 7038164000
;             TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: genomic DNA
;        HYPOTHETICAL: YES
;        FEATURE:
;             NAME/KEY:  misc_RNA
;             LOCATION:  1..9
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-290-736C-12

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
              |||||||
Db          9 CATGGAT 3


RESULT 101
US-09-479-005A-1198/c
; Sequence 1198, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-C
;  CURRENT APPLICATION NUMBER: US/09/479,005A
;  CURRENT FILING DATE:  2000-01-07
;  PRIOR APPLICATION NUMBER: US 09/444,209
;  PRIOR FILING DATE: 1999-11-19
;  PRIOR APPLICATION NUMBER: US 09/159,274
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: US 60/059,473
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 1208
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1198
;   LENGTH: 9
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Substrate Nucleic Acid for SI
;   OTHER INFORMATION: NO: 1197
US-09-479-005A-1198

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATG 7
              |||||||
Db          8 CCTCATG 2


RESULT 102
US-10-096-596-12/c
; Sequence 12, Application US/10096596
; Patent No. 6746845
; GENERAL INFORMATION:
;  APPLICANT: Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  APPLICANT:  Velculescu, Victor
;  APPLICANT:  Zhang, Lin
;  TITLE OF INVENTION: METHOD FOR SERIAL ANLAYSIS OF GENE EXPRESSION
;  FILE REFERENCE: 001107.00242
;  CURRENT APPLICATION NUMBER: US/10/096,596
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: US 08/527,154
;  PRIOR FILING DATE: 1995-09-12
;  PRIOR APPLICATION NUMBER: US 08/544,861
;  PRIOR FILING DATE: 1995-10-18
;  PRIOR APPLICATION NUMBER: US 09/107,228
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-096-596-12

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGGTCAC 12
              |||||||
Db          9 TGGTCAC 3


RESULT 103
US-10-209-059-40/c
; Sequence 40, Application US/10209059
; Patent No. 6930225
; GENERAL INFORMATION:
;  APPLICANT: Dhugga, Kanwarpal S.
```

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;  APPLICANT:  Wang, Haiyin
;  TITLE OF INVENTION: Maize Cellulose Synthases and Uses
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 0864R2
;  CURRENT APPLICATION NUMBER: US/10/209,059
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: 60/096,822
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 09/371,383
;  PRIOR FILING DATE: 1999-08-06
;  PRIOR APPLICATION NUMBER: 09/550,483
;  PRIOR FILING DATE: 2000-04-14
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Zea mays
US-10-209-059-40

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CACATGG 16
               |||||||
Db          8 CACATGG 2


RESULT 104
US-09-990-186-2103
; Sequence 2103, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2103
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2103

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGGATGA 20
               |||||||
Db          2 TGGATGA 8


RESULT 105
US-07-874-334-2
; Sequence 2, Application US/07874334
; Patent No. 5495009
;  GENERAL INFORMATION:
;    APPLICANT:  MATTEUCCI, MARK
;    APPLICANT:  JONES, BOB
;    APPLICANT:  LIN, KUEI-YING
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE ANALOGS CONTAINING
;    TITLE OF INVENTION:  THIOFORMACETAL LINKAGES
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/874,334
;      FILING DATE:  19920424
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24610-20005.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-874-334-2

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 ATGGTCA 11
               |||||||
Db          1 ATGGTCA 7


RESULT 106
US-08-174-672D-113
; Sequence 113, Application US/08174672D
; Patent No. 5877009
;  GENERAL INFORMATION:
;    APPLICANT:  Zannis Ph.D., Vassilis I.
;    APPLICANT:  Cladaras Ph.D., Christos
;    TITLE OF INVENTION:  APOLIPOPROTEIN GENE REGULATION
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Choate, Hall & Stewart
;      STREET:  53 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2891
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/174,672D
;      FILING DATE:  28-DEC-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jarrell Ph.D., Brenda H.
;      REGISTRATION NUMBER:  39,223
;      REFERENCE/DOCKET NUMBER:  0079571-0005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
;      TELEFAX:  (617) 248 4000
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      STRAIN:  BamHl linker
US-08-174-672D-113

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
               |||||||
Db          2 CATGGAT 8


RESULT 107
US-08-465-794-12
; Sequence 12, Application US/08465794
; Patent No. 5886141
;  GENERAL INFORMATION:
;    APPLICANT:  FOLKMAN, MOSES J.
;    APPLICANT:  SHING, YUEN
;    APPLICANT:  IGARASHI, KOICHI
;    TITLE OF INVENTION:  SMOOTH MUSCLE MITOGEN AND ISOLATED DNA
;    TITLE OF INVENTION:  CODING THEREFORE
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,794
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/007,126
;      FILING DATE:  21-JAN-1993
;      APPLICATION NUMBER:  US 07/994,776
;      FILING DATE:  22-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,597
;      FILING DATE:  23-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,792
;      FILING DATE:  23-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/833,552
;      FILING DATE:  10-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/832,939
;      FILING DATE:  10-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/766,354
;      FILING DATE:  26-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/604,778
;      FILING DATE:  26-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RESNICK, DAVID S.
;      REGISTRATION NUMBER:  34235
;      REFERENCE/DOCKET NUMBER:  40435-CIP-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-465-794-12

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
               |||||||
Db          2 ATGGATG 8


RESULT 108
US-08-822-701-5/c
; Sequence 5, Application US/08822701
; Patent No. 5976853
;  GENERAL INFORMATION:
;    APPLICANT:  Guthridge, Mark
;    APPLICANT:  Basilico, Claudio
;    TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;    TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,701
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-002 N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-822-701-5

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGT 9
              |||||||
```

```
Db         10 TCATGGT 4


RESULT 109
US-08-469-461-7/c
; Sequence 7, Application US/08469461B
; Patent No. 5981178
; GENERAL INFORMATION:
;  APPLICANT: Tsui, Lap-Chee
;  APPLICANT: Rommins, Johanna M.
;  APPLICANT: Kerem, Bat-Sheva
;  TITLE OF INVENTION: Introns and Exons of the Cystic Fibrosis Gene and
;  TITLE OF INVENTION: Mutations at Various Positions of the Gene
;  FILE REFERENCE: 3477-61, 033477/139840
;  CURRENT APPLICATION NUMBER: US/08/469,461B
;  CURRENT FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;    LENGTH: 10
;    TYPE: RNA
;    ORGANISM: Homo sapiens
US-08-469-461-7

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CATGGTC 10
              |||||||
Db          8 CATGGTC 2


RESULT 110
US-08-724-354D-12/c
; Sequence 12, Application US/08724354D
; Patent No. 5994119
;  GENERAL INFORMATION:
;    APPLICANT:  Dietz, Harry C.
;    TITLE OF INVENTION:  MAMMALIAN REGULATOR OF
;    TITLE OF INVENTION:  NONSENSE-MEDIATED RNA DECAY
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  4225 Excutive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,354D
;      FILING DATE:  01-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/016,482
;      FILING DATE:  29-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/090001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-678-5070
;      TELEFAX:  619-678-5099
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-724-354D-12

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGT 9
              |||||||
Db         10 TCATGGT 4


RESULT 111
US-07-890-609-7/c
; Sequence 7, Application US/07890609C
; Patent No. 6001588
; GENERAL INFORMATION:
;  APPLICANT: Tsui, Lap-Chee
;  APPLICANT: Rommins, Johanna M.
;  APPLICANT: Kerem, Bat-Sheva
;  TITLE OF INVENTION: Introns and Exons of the Cystic Fibrosis Gene and
;  TITLE OF INVENTION: Mutations at Various Positions of the Gene
;  FILE REFERENCE: 3477-61, 033477/139840
;  CURRENT APPLICATION NUMBER: US/07/890,609C
;  CURRENT FILING DATE: 1992-07-13
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;    LENGTH: 10
;    TYPE: RNA
;    ORGANISM: Homo sapiens
US-07-890-609-7

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CATGGTC 10
              |||||||
Db          8 CATGGTC 2


RESULT 112
US-08-388-353-115
; Sequence 115, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  115:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-115

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGA 17
               |||||||
Db           4 ACATGGA 10


RESULT 113
US-08-388-353-116
; Sequence 116, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  116:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-116

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGA 17
               |||||||
Db           3 ACATGGA 9


RESULT 114
US-08-388-353-117
; Sequence 117, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  117:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-117

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGA 17
               |||||||
Db           2 ACATGGA 8


RESULT 115
US-08-388-353-118
; Sequence 118, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
```

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;       STATE:  New York
;       COUNTRY:  United States
;       ZIP:  11530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/388,353
;       FILING DATE:  14-FEB-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DiGiglio, Frank S.
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  9606
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (516) 742-4343
;       TELEFAX:  (516) 742-4366
;       TELEX:  230 901 SANS UR
;   INFORMATION FOR SEQ ID NO:  118:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-388-353-118

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 ACATGGA 17
               |||||||
Db          1 ACATGGA 7


RESULT 116
US-08-388-353-515
; Sequence 515, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  515:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-515

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
               |||||||
Db          4 ATGGATG 10


RESULT 117
US-08-388-353-519
; Sequence 519, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  519:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-519

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGGATGA 20
               |||||||
Db          1 TGGATGA 7
```

```
RESULT 118
US-09-049-813-12
; Sequence 12, Application US/09049813
; Patent No. 6013762
;  GENERAL INFORMATION:
;    APPLICANT:  FOLKMAN, MOSES J.
;    APPLICANT:  SHING, YUEN
;    APPLICANT:  IGARASHI, KOICHI
;    TITLE OF INVENTION:  SMOOTH MUSCLE MITOGEN AND ISOLATED DNA
;    TITLE OF INVENTION:  CODING THEREFORE
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/049,813
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,794
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/007,126
;      FILING DATE:  21-JAN-1993
;      APPLICATION NUMBER:  US 07/994,776
;      FILING DATE:  22-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,597
;      FILING DATE:  23-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,792
;      FILING DATE:  23-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/833,552
;      FILING DATE:  10-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/832,939
;      FILING DATE:  10-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/766,354
;      FILING DATE:  26-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/604,778
;      FILING DATE:  26-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RESNICK, DAVID S.
;      REGISTRATION NUMBER:  34235
;      REFERENCE/DOCKET NUMBER:  40435-CIP-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-09-049-813-12

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATG 19
               |||||||
Db           2 ATGGATG 8


RESULT 119
US-08-488-551B-115
; Sequence 115, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  115:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-115

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGA 17
               |||||||
Db           4 ACATGGA 10


RESULT 120
US-08-488-551B-116
; Sequence 116, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
```

```
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  116:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-116

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 ACATGGA 17
               |||||||
Db          3 ACATGGA 9


RESULT 121
US-08-488-551B-117
; Sequence 117, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  117:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-117

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 ACATGGA 17
               |||||||
Db          2 ACATGGA 8


RESULT 122
US-08-488-551B-118
; Sequence 118, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
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;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  118:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-118

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 ACATGGA 17
               |||||||
Db          1 ACATGGA 7


RESULT 123
US-08-488-551B-515
; Sequence 515, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  515:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-515

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
               |||||||
Db          4 ATGGATG 10


RESULT 124
US-08-488-551B-519
; Sequence 519, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  519:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-519

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGGATGA 20
               |||||||
Db          1 TGGATGA 7
```

```
RESULT 125
US-08-488-551B-833
; Sequence 833, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  833:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-833

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATG 19
               |||||||
Db           4 ATGGATG 10


RESULT 126
US-08-488-551B-837
; Sequence 837, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  837:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-837

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 TGGATGA 20
               |||||||
Db           1 TGGATGA 7


RESULT 127
US-09-270-984A-12/c
; Sequence 12, Application US/09270984A
; Patent No. 6048965
;  GENERAL INFORMATION:
;    APPLICANT:  Dietz, Harry C.
;    TITLE OF INVENTION:  MAMMALIAN REGULATOR OF
;    TITLE OF INVENTION:  NONSENSE-MEDIATED RNA DECAY
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  4225 Excutive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/270,984A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  08/724,354
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/090001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-678-5070
;      TELEFAX:  619-678-5099
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-270-984A-12

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGT 9
              |||||||
Db         10 TCATGGT 4


RESULT 128
US-08-872-417B-4
; Sequence 4, Application US/08872417B
; Patent No. 6066470
;  GENERAL INFORMATION:
;    APPLICANT:  Nishimura, Osamu
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Ohmae, Hiroaki
;    APPLICANT:  Tsuji, Shinji
;    TITLE OF INVENTION:  Method of Removing N-terminal
;    TITLE OF INVENTION:  Methionine
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dike, Bronstein, Roberts & Cushman, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/872,417B
;      FILING DATE:  10-JUN-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JA 154634/96
;      FILING DATE:  14-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  47423
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-872-417B-4

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
              |||||||
Db          2 ATGGATG 8


RESULT 129
US-08-935-855-5/c
; Sequence 5, Application US/08935855
; Patent No. 6066485
;  GENERAL INFORMATION:
;    APPLICANT:  Guthridge, Mark
;    APPLICANT:  Basilico, Claudio
;    TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;    TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,855
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-002 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-935-855-5

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGT 9
              |||||||
Db         10 TCATGGT 4


RESULT 130
US-09-063-450-32/c
; Sequence 32, Application US/09063450
; Patent No. 6109776
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: Method and System for Computationally Identifying
;  TITLE OF INVENTION: Clusters Within a Set of Sequences
;  FILE REFERENCE: 77001.002
;  CURRENT APPLICATION NUMBER: US/09/063,450
```

```
;  CURRENT FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:example
;   OTHER INFORMATION: sequence illustrating a computational methodology
US-09-063-450-32

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGA 17
               |||||||
Db           7 ACATGGA 1


RESULT 131
US-08-729-601A-67
; Sequence 67, Application US/08729601A
; Patent No. 6166302
;  GENERAL INFORMATION:
;    APPLICANT:  Merlo, Donald J.
;    APPLICANT:  Folkerts, Otto
;    TITLE OF INVENTION:  Modified Bacillus Thuringiensis Gene for
;    TITLE OF INVENTION:  Lepidopteran Control in Plants
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 S. LaSalle St.
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/729,601A
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Krueger, James P.
;      REGISTRATION NUMBER:  35,234
;      REFERENCE/DOCKET NUMBER:  60089
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-372-7842
;      TELEFAX:  312-372-7848
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-729-601A-67

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CATGGAT 18
               |||||||
Db           1 CATGGAT 7


RESULT 132
US-08-988-321B-29
; Sequence 29, Application US/08988321B
; Patent No. 6174868
;  GENERAL INFORMATION:
;    APPLICANT:  Kevin P. Anderson et al.
;    TITLE OF INVENTION:  Compositions And Methods For Treatment  Of Hepatitis C V
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Jane Massey Licata
;      STREET:  66 East Main Street
;      CITY:  Marlton
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM COMPATIBLE
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WORDPERFECT 6.1 FOR WINDOWS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,321B
;      FILING DATE:  December 10, 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/650,093
;      FILING DATE:  May 17, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/452,841
;      FILING DATE:  May 30, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/397,220
;      FILING DATE:  March 9, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/945,289
;      FILING DATE:  September 10, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  ISPH-0245
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (856) 810-1515
;      TELEFAX:  (856) 810-1454
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10
;      TYPE:  nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  Yes
US-08-988-321B-29

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 CTCATGG 8
               |||||||
Db           4 CTCATGG 10


RESULT 133
US-08-663-191A-5
; Sequence 5, Application US/08663191A
; Patent No. 6183971
;  GENERAL INFORMATION:
;       APPLICANT: Reiko SASADA, et al.
;       TITLE OF INVENTION: ANTIBODY, HYBRIDOMA AND USE THEREOF
;       NUMBER OF SEQUENCES: 10
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
;            STREET: 2033 K Street, N.W., Suite 800
;            CITY: Washington
;            STATE: D.C.
```

```
;            COUNTRY: U.S.A.
;            ZIP: 20006
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: MS-DOS
;            SOFTWARE: Wordperfect 5.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/663,191A
;            FILING DATE: 11-Jun-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Lee Cheng
;            REGISTRATION NUMBER: 40,949
;            REFERENCE/DOCKET NUMBER: 96-0256/LC(WMC)/927
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-721-8200
;            TELEFAX: 202-721-8250
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-663-191A-5

  Query Match            35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
               |||||||
Db          2 ATGGATG 8


RESULT 134
US-08-991-789A-100/c
; Sequence 100, Application US/08991789A
; Patent No. 6225054
;   GENERAL INFORMATION:
;       APPLICANT: Frudakis, Tony N.
;                  Smith, John M.
;                  Reed, Steven G.
;       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;                           TREATMENT AND DIAGNOSIS OF BREAST CANCER
;       NUMBER OF SEQUENCES: 292
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed IP Law Group
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/991,789A
;            FILING DATE: 11-Dec-1997
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Potter, Jane E. R.
;            REGISTRATION NUMBER: 33,332
;            REFERENCE/DOCKET NUMBER: 210121.419C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 100:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-08-991-789A-100

  Query Match            35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
               |||||||
Db          9 CATGGAT 3


RESULT 135
US-09-436-518-4
; Sequence 4, Application US/09436518
; Patent No. 6309859
; GENERAL INFORMATION:
;  APPLICANT: NISHIMURA, OSAMU
;  APPLICANT:  SUENAGA, MASATO
;  APPLICANT:  OHMAE, HIROAKI
;  APPLICANT:  TSUJI, SHINJI
;  TITLE OF INVENTION: METHOD FOR REMOVING N-TERMINAL METHIONINE
;  FILE REFERENCE: 47423-CPA-CON (342)
;  CURRENT APPLICATION NUMBER: US/09/436,518
;  CURRENT FILING DATE:  1999-11-09
;  PRIOR APPLICATION NUMBER: 08/872,417
;  PRIOR FILING DATE: 1997-06-10
;  PRIOR APPLICATION NUMBER: JP 8-154634
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: adapter
US-09-436-518-4

  Query Match            35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
               |||||||
Db          2 ATGGATG 8


RESULT 136
US-08-623-428D-34
; Sequence 34, Application US/08623428D
; Patent No. 6312890
;   GENERAL INFORMATION:
;       APPLICANT: W. MARSTON LINEHAN, MICHAEL
;                  LERMAN, FARIDA LATIF AND BERTON
;                  ZBAR
;       TITLE OF INVENTION: PARTIAL INTRON SEQUENCE
;                           OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS
;                           OF DISEASE CARRIERS
;       NUMBER OF SEQUENCES: 63
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;            STREET: 345 PARK AVENUE
;            CITY: NEW YORK
;            STATE: NEW YORK
```

```
;          COUNTRY: USA
;          ZIP: 10154
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: FLOPPY DISK
;          COMPUTER: IBM PC COMPATIBLE
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: MICROSOFT WORD 97
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/623,428D
;          FILING DATE: 05-Sep-2000
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/623,428
;          FILING DATE: MARCH 28, 1996
;          APPLICATION NUMBER: 08/061,889
;          FILING DATE: May 14, 1993
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Kathryn M. Brown
;          REGISTRATION NUMBER: 34,556
;          REFERENCE/DOCKET NUMBER: 2026-4078US3
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 758-4800
;          TELEFAX: (212) 751-6849
;          TELEX: 421792
;   INFORMATION FOR SEQ ID NO: 34:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 10 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-623-428D-34

  Query Match            35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGGTCAC 12
              |||||||
Db          4 TGGTCAC 10


RESULT 137
US-09-062-451-100/c
; Sequence 100, Application US/09062451
; Patent No. 6344550
;  GENERAL INFORMATION:
;    APPLICANT:  Frudakis, Tony N.
;    APPLICANT:  Smith, John M.
;    APPLICANT:  Reed, Steven G.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF BREAST CANCER
;    NUMBER OF SEQUENCES:  297
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/062,451
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.419C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-062-451-100

  Query Match            35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CATGGAT 18
               |||||||
Db           9 CATGGAT 3


RESULT 138
US-08-650-093C-112
; Sequence 112, Application US/08650093C
; Patent No. 6391542
;  GENERAL INFORMATION:
;       APPLICANT: Kevin P. Anderson et al.
;       TITLE OF INVENTION: Compositions And Methods For Treatment  Of
;                           Hepatitis C Virus-Associated Diseases
;       NUMBER OF SEQUENCES: 118
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: LICATA & TYRRELL P.C.
;          STREET: 66 E. Main Street
;          CITY: Marlton
;          STATE: NJ
;          COUNTRY: USA
;          ZIP: 08053
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;          COMPUTER: IBM Compatible
;          OPERATING SYSTEM: Windows 95
;          SOFTWARE: WORDPERFECT 6.1 for Windows
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/650,093C
;          FILING DATE: 17-May-1996
;          CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/452,841
;          FILING DATE: May 30, 1995
;          APPLICATION NUMBER: 08/397,220
;          FILING DATE: March 9, 1995
;          APPLICATION NUMBER: 07/945,289
;          FILING DATE: September 10, 1992
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Jane Massey Licata
;          REGISTRATION NUMBER: 32,257
;          REFERENCE/DOCKET NUMBER: ISPH-
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (609) 779-2400
;          TELEFAX: (609) 779-8488
;  INFORMATION FOR SEQ ID NO: 112:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 10
;          TYPE: Nucleic Acid
;          STRANDEDNESS: Single
;          TOPOLOGY: Linear
;       ANTI-SENSE: Yes
;       SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-08-650-093C-112

  Query Match            35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          2 CTCATGG 8
              |||||||
Db          4 CTCATGG 10


RESULT 139
US-09-598-326-100/c
; Sequence 100, Application US/09598326
; Patent No. 6423496
;  GENERAL INFORMATION:
;       APPLICANT: Frudakis, Tony N.
;                  Smith, John M.
;                  Reed, Steven G.
;       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;                           TREATMENT AND DIAGNOSIS OF BREAST CANCER
;       NUMBER OF SEQUENCES: 247
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group PLLC
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/598,326
;            FILING DATE: 20-Jun-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Potter, Jane E.R.
;            REGISTRATION NUMBER: 33,332
;            REFERENCE/DOCKET NUMBER: 210121.419D1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 100:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-598-326-100

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
              |||||||
Db          9 CATGGAT 3


RESULT 140
US-09-508-753B-132
; Sequence 132, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 132
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-132

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGGATGA 20
              |||||||
Db          1 TGGATGA 7


RESULT 141
US-09-289-198-100/c
; Sequence 100, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
;  APPLICANT: Frudakis, Tony N.
;  APPLICANT: Smith, John M.
;  APPLICANT: Reed, Steven G.
;  APPLICANT: Misher, Lynda
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.419C5
;  CURRENT APPLICATION NUMBER: US/09/289,198
;  CURRENT FILING DATE: 1999-04-09
;  EARLIER APPLICATION NUMBER: US 09/062,451
;  EARLIER FILING DATE: 1998-04-17
;  EARLIER APPLICATION NUMBER: US 08/991,789
;  EARLIER FILING DATE: 1997-12-11
;  EARLIER APPLICATION NUMBER: US 08/838,762
;  EARLIER FILING DATE: 1997-04-09
;  EARLIER APPLICATION NUMBER: PCT/US97/00485
;  EARLIER FILING DATE: 1997-01-10
;  EARLIER APPLICATION NUMBER: US 08/700,014
;  EARLIER FILING DATE: 1996-08-20
;  EARLIER APPLICATION NUMBER: US 08/585,392
;  EARLIER FILING DATE: 1996-01-01
;  NUMBER OF SEQ ID NOS: 312
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 100
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-289-198-100

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
              |||||||
Db          9 CATGGAT 3


RESULT 142
US-09-690-936-29
; Sequence 29, Application US/09690936
; Patent No. 6608191
; GENERAL INFORMATION:
;  APPLICANT:  Anderson, Kevin P.
;  APPLICANT:  Hanecak, Ronnie C.
;  APPLICANT:  No. 6608191aki, Chikateru
;  TITLE OF INVENTION:  Compositions and Methods for Treatment of Hepatitis C
```

```
;  TITLE OF INVENTION:  Virus-Associated Disease
;  FILE REFERENCE:  ISPH-0517
;  CURRENT APPLICATION NUMBER: US/09/690,936
;  CURRENT FILING DATE:  2000-10-18
;  PRIOR APPLICATION NUMBER:  08/988,321
;  PRIOR FILING DATE:  1997-12-10
;  PRIOR APPLICATION NUMBER:  08/650,093
;  PRIOR FILING DATE:  1996-05-17
;  PRIOR APPLICATION NUMBER:  08/452,841
;  PRIOR FILING DATE:  1995-05-30
;  PRIOR APPLICATION NUMBER:  08/397,330
;  PRIOR FILING DATE:  1995-03-09
;  PRIOR APPLICATION NUMBER:  07/945,289
;  PRIOR FILING DATE:  1992-09-10
;  NUMBER OF SEQ ID NOS:  37
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-690-936-29

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGG 8
              |||||||
Db          4 CTCATGG 10


RESULT 143
US-09-429-755-100/c
; Sequence 100, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
;  APPLICANT:  Frudakis, Tony N.
;  APPLICANT:  Smith, John M.
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Misher, Lynda
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Dillon, Davin C.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.419C6
;  CURRENT APPLICATION NUMBER: US/09/429,755A
;  CURRENT FILING DATE:  1999-10-28
;  NUMBER OF SEQ ID NOS:  315
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 100
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-429-755-100

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
              |||||||
Db          9 CATGGAT 3


RESULT 144
US-09-995-973-12/c
; Sequence 12, Application US/09995973
; Patent No. 6706470
; GENERAL INFORMATION:
;  APPLICANT: CHOO, Yen
;  APPLICANT:  ULLMAN, Christopher G.
;  TITLE OF INVENTION: GENE SWITCHES
;  FILE REFERENCE: 8325-2003 / G7-US1
;  CURRENT APPLICATION NUMBER: US/09/995,973
;  CURRENT FILING DATE:  2002-03-19
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  plant
;   OTHER INFORMATION: translational initiation sequence
US-09-995-973-12

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CATGGTC 10
              |||||||
Db         10 CATGGTC 4


RESULT 145
US-09-822-250A-16
; Sequence 16, Application US/09822250A
; Patent No. 6706477
; GENERAL INFORMATION:
;  APPLICANT: Zauderer, Maurice
;  TITLE OF INVENTION: Methods for Producing Polynucleotide Libraries in Vaccinia Virus
;  FILE REFERENCE: 1821.0010001
;  CURRENT APPLICATION NUMBER: US/09/822,250A
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 08/935,377
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MR_15 primer
US-09-822-250A-16

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACAT 14
              |||||||
Db          2 GTCACAT 8


RESULT 146
US-09-822-250A-17
; Sequence 17, Application US/09822250A
; Patent No. 6706477
; GENERAL INFORMATION:
;  APPLICANT: Zauderer, Maurice
;  TITLE OF INVENTION: Methods for Producing Polynucleotide Libraries in Vaccinia Virus
;  FILE REFERENCE: 1821.0010001
;  CURRENT APPLICATION NUMBER: US/09/822,250A
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 08/935,377
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 10
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MR_9 primer
US-09-822-250A-17

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACA 13
              |||||||
Db          3 GGTCACA 9


RESULT 147
US-09-806-871A-7
; Sequence 7, Application US/09806871A
; Patent No. 6774221
; GENERAL INFORMATION:
;  APPLICANT: NISHIMURA, Osamu
;  TITLE OF INVENTION: METHOD FOR REMOVING N-TERMINAL METHIONINE
;  FILE REFERENCE: 2001-0291A/WMC/01801
;  CURRENT APPLICATION NUMBER: US/09/806,871A
;  CURRENT FILING DATE:  2001-04-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: DNA PRIMER
US-09-806-871A-7

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATG 19
              |||||||
Db          2 ATGGATG 8


RESULT 148
US-10-034-350A-16
; Sequence 16, Application US/10034350A
; Patent No. 6800442
; GENERAL INFORMATION:
;  APPLICANT: Zauderer, Maurice
;  TITLE OF INVENTION: Methods of Selecting Polynucleotides Encoding Antigens
;  FILE REFERENCE: 1821.0010002
;  CURRENT APPLICATION NUMBER: US/10/034,350A
;  CURRENT FILING DATE:  2002-01-03
;  PRIOR APPLICATION NUMBER: US 08/935,377
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-034-350A-16

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACAT 14
              |||||||
Db          2 GTCACAT 8


RESULT 149
US-10-034-350A-17
; Sequence 17, Application US/10034350A
; Patent No. 6800442
; GENERAL INFORMATION:
;  APPLICANT: Zauderer, Maurice
;  TITLE OF INVENTION: Methods of Selecting Polynucleotides Encoding Antigens
;  FILE REFERENCE: 1821.0010002
;  CURRENT APPLICATION NUMBER: US/10/034,350A
;  CURRENT FILING DATE:  2002-01-03
;  PRIOR APPLICATION NUMBER: US 08/935,377
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-034-350A-17

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACA 13
              |||||||
Db          3 GGTCACA 9


RESULT 150
US-09-699-295-100/c
; Sequence 100, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
;  APPLICANT:  Frudakis, Tony N.
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Smith, John M.
;  APPLICANT:  Misher, Linda E.
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.419C10
;  CURRENT APPLICATION NUMBER: US/09/699,295
;  CURRENT FILING DATE:  2000-10-26
;  NUMBER OF SEQ ID NOS:  326
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 100
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-699-295-100

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
              |||||||
Db          9 CATGGAT 3


RESULT 151
US-09-534-825A-100/c
```

```
; Sequence 100, Application US/09534825A
; Patent No. 6861506
; GENERAL INFORMATION:
;  APPLICANT:  Frudakis, Tony N.
;  APPLICANT:  Smith, John M.
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Misher, Lynda
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Dillon, Davin C.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.419C7
;  CURRENT APPLICATION NUMBER: US/09/534,825A
;  CURRENT FILING DATE:  2000-03-23
;  NUMBER OF SEQ ID NOS:  317
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 100
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-534-825A-100

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CATGGAT 18
               |||||||
Db           9 CATGGAT 3


RESULT 152
US-08-935-377-16
; Sequence 16, Application US/08935377
; Patent No. 6872518
;  GENERAL INFORMATION:
;    APPLICANT:  Zauderer, Maurice
;    TITLE OF INVENTION:  T Cells Specific for Target Antigens and
;    TITLE OF INVENTION:  Vaccines Based Thereon
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,377
;      FILING DATE:  22-SEP-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1821.0010000/EKS/CMB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-935-377-16

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           8 GTCACAT 14
               |||||||
Db           2 GTCACAT 8


RESULT 153
US-08-935-377-17
; Sequence 17, Application US/08935377
; Patent No. 6872518
;  GENERAL INFORMATION:
;    APPLICANT:  Zauderer, Maurice
;    TITLE OF INVENTION:  T Cells Specific for Target Antigens and
;    TITLE OF INVENTION:  Vaccines Based Thereon
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,377
;      FILING DATE:  22-SEP-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1821.0010000/EKS/CMB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-935-377-17

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           7 GGTCACA 13
               |||||||
Db           3 GGTCACA 9


RESULT 154
US-09-910-469-75/c
; Sequence 75, Application US/09910469
; Patent No. 6893822
; GENERAL INFORMATION:
;  APPLICANT: Schweitzer, Markus
;  APPLICANT:  Anderson, Richard R.
;  APPLICANT:  Mueller, Jochen
;  APPLICANT:  Fiechtner, Michael
;  APPLICANT:  Bruecher, Christoph
;  APPLICANT:  Kienle, Stefan
;  APPLICANT:  Orwick, Jill
;  APPLICANT:  Pignot, Marc
```

```
;  APPLICANT:  Raddatz, Stefan
;  APPLICANT:  Schneider, Eberhard
;  APPLICANT:  Windhab, No. 6893822bert
;  TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthet
;  TITLE OF INVENTION:  Binding Systems
;  FILE REFERENCE: 264/217 Nanogen Recognomics
;  CURRENT APPLICATION NUMBER: US/09/910,469
;  CURRENT FILING DATE:  2001-07-19
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic binding system
;   NAME/KEY: modified_base
;   LOCATION: (1)..(10)
;   OTHER INFORMATION: pyranosyl RNA
US-09-910-469-75

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGA 17
               |||||||
Db           8 ACATGGA 2


RESULT 155
US-09-910-469-76
; Sequence 76, Application US/09910469
; Patent No. 6893822
; GENERAL INFORMATION:
;  APPLICANT: Schweitzer, Markus
;  APPLICANT:  Anderson, Richard R.
;  APPLICANT:  Mueller, Jochen
;  APPLICANT:  Fiechtner, Michael
;  APPLICANT:  Bruecher, Christoph
;  APPLICANT:  Kienle, Stefan
;  APPLICANT:  Orwick, Jill
;  APPLICANT:  Pignot, Marc
;  APPLICANT:  Raddatz, Stefan
;  APPLICANT:  Schneider, Eberhard
;  APPLICANT:  Windhab, No. 6893822bert
;  TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthet
;  TITLE OF INVENTION:  Binding Systems
;  FILE REFERENCE: 264/217 Nanogen Recognomics
;  CURRENT APPLICATION NUMBER: US/09/910,469
;  CURRENT FILING DATE:  2001-07-19
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic binding system
;   NAME/KEY: modified_base
;   LOCATION: (1)..(10)
;   OTHER INFORMATION: pyranosyl RNA
US-09-910-469-76

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGA 17
               |||||||
Db           3 ACATGGA 9


RESULT 156
US-08-252-778-46/c
; Sequence 46, Application US/08252778
; Patent No. 6902907
; GENERAL INFORMATION:
;  APPLICANT: Tsui, Lap-Chee
;  APPLICANT:  Riordan, John R.
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Kerem, Bat-Sheva
;  APPLICANT:  Buchwald, Manuel
;  APPLICANT:  Collins, Francis S.
;  APPLICANT:  Iannuzzi, Michael C.
;  APPLICANT:  Drumm, Mitchell L.
;  TITLE OF INVENTION: Cystic Fibrosis Gene
;  FILE REFERENCE: 1329.0010004
;  CURRENT APPLICATION NUMBER: US/08/252,778
;  CURRENT FILING DATE:  1994-06-02
;  PRIOR APPLICATION NUMBER: US 08/123,864
;  PRIOR FILING DATE: 1993-09-20
;  PRIOR APPLICATION NUMBER: US 07/401,609
;  PRIOR FILING DATE: 1989-08-31
;  PRIOR APPLICATION NUMBER: US 07/399,945
;  PRIOR FILING DATE: 1989-08-24
;  PRIOR APPLICATION NUMBER: US 07/396,894
;  PRIOR FILING DATE: 1989-08-22
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence containing start codon in combined cDNA
; Patent No. 6902907
US-08-252-778-46

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           4 CATGGTC 10
               |||||||
Db           8 CATGGTC 2


RESULT 157
US-09-977-615B-54
; Sequence 54, Application US/09977615B
; Patent No. 6977161
; GENERAL INFORMATION:
;  APPLICANT: EraGen Biosciences, Inc.
;  APPLICANT:  Grenier, Jennifer
;  APPLICANT:  Marshall, David
;  APPLICANT:  Prudent, James
;  APPLICANT:  Richmond, Craig
;  APPLICANT:  Roesch, Eric
;  APPLICANT:  Scherrer, Christopher
;  APPLICANT:  Sherrill, Christopher
;  APPLICANT:  Ptacin, Jerod
;  TITLE OF INVENTION: Solid Support Assay Systems and Methods Utilizing No. 6977161-Natu
;  TITLE OF INVENTION:  Bases
;  FILE REFERENCE: PAT015-US5
;  CURRENT APPLICATION NUMBER: US/09/977,615B
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 60/240,397
;  PRIOR FILING DATE: 2000-10-14
;  PRIOR APPLICATION NUMBER: 60/282,831
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 09/861,292
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: 60/293,259
;  PRIOR FILING DATE: 2001-05-22
;  NUMBER OF SEQ ID NOS: 165
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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: n represents iso-cytosine
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: n represents iso-cytosine
US-09-977-615B-54

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGT 9
              ||| ||||
Db          1 CTCNTGGT 8


RESULT 158
US-10-111-708-6
; Sequence 6, Application US/10111708
; Patent No. 6995010
; GENERAL INFORMATION:
;  APPLICANT: UENO, Takashi
;  APPLICANT:  MATSUMURA, Hajime
;  APPLICANT:  TANAKA, Keiji
;  APPLICANT:  IWASAKI, Tomoko
;  APPLICANT:  UENO, Mitsuhiro
;  APPLICANT:  FUJINAGA, Kei
;  APPLICANT:  ASADA, Kiyozo
;  APPLICANT:  KATO, Ikunoshin
;  TITLE OF INVENTION: GENE TRANSFER METHOD
;  FILE REFERENCE: UENO=9
;  CURRENT APPLICATION NUMBER: US/10/111,708
;  CURRENT FILING DATE:  2000-10-23
;  PRIOR APPLICATION NUMBER: PCT JP00 07373
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: JP 11/308839
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: EcoRV linker
US-10-111-708-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
              |||||||
Db          1 CATGGAT 7


RESULT 159
US-09-853-409-29
; Sequence 29, Application US/09853409
; Patent No. 6995146
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Kevin P.
;  APPLICANT:  Hanecak, Ronnie C.
;  APPLICANT:  No. 6995146aki, Chikateru
;  APPLICANT:  Dorr, F. Andrew
;  APPLICANT:  Kwoh, T. Jesse
;  TITLE OF INVENTION: Compositions and Methods for Treatment of Hepatitis C
;  TITLE OF INVENTION:  Virus-Associated Disease
;  FILE REFERENCE: ISPH-0569
;  CURRENT APPLICATION NUMBER: US/09/853,409
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 08/988,321
;  PRIOR FILING DATE: 1997-12-10
;  PRIOR APPLICATION NUMBER: 08/650,093
;  PRIOR FILING DATE: 1996-05-17
;  PRIOR APPLICATION NUMBER: 08/452,841
;  PRIOR FILING DATE: 1995-05-30
;  PRIOR APPLICATION NUMBER: 08/397,330
;  PRIOR FILING DATE: 1995-03-09
;  PRIOR APPLICATION NUMBER: 07/945,289
;  PRIOR FILING DATE: 1992-09-10
;  PRIOR APPLICATION NUMBER: 09/690,936
;  PRIOR FILING DATE: 2000-10-18
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-853-409-29

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGG 8
              |||||||
Db          4 CTCATGG 10


RESULT 160
US-09-030-832-23/c
; Sequence 23, Application US/09030832
; Patent No. 7029870
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-030-832-23

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 ATGGTCA 11
              |||||||
Db          9 ATGGTCA 3


RESULT 161
5470721-7/c
;Patent No. 5470721
;    APPLICANT: BUELL, GARY N.;MOVVA, NAAGESWARARAO
;    TITLE OF INVENTION: PRODUCTION OF HUMAN SOMATOMEDIN C
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/81,979
;      FILING DATE: 23-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 965,047
;      FILING DATE: 21-OCT-1992
;      APPLICATION NUMBER: 496,086
;      FILING DATE: 15-MAR-1990
;      APPLICATION NUMBER: 938,170
;      FILING DATE: 19-NOV-1986
;SEQ ID NO:7:
;      LENGTH: 10
5470721-7

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGAT 18
              |||||||
Db          9 CATGGAT 3


RESULT 162
5256545-14/c
;Patent No. 5256545
;    APPLICANT: BROWN, MICHAEL S.;GOLDSTEIN, JOSEPH L.;RUSSELL,
;DAVID W.;SUDHOF, THOMAS C.
;    TITLE OF INVENTION: STEROL REGULATORY ELEMENTS
;    NUMBER OF SEQUENCES: 42
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/425,852
;      FILING DATE: 20-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 33,330
;      FILING DATE: 30-MAR-1987
;      APPLICATION NUMBER: 33,081
;      FILING DATE: 30-MAR-1987
;SEQ ID NO:14:
;      LENGTH: 10
5256545-14

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 72;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              |||| |||
Db          8 CATGCATG 1


Search completed: November 22, 2006, 14:05:03
Job time : 1 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 13:59:33 ; Search time 0.001 Seconds
(without alignments)
92.160 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 191 seqs, 2304 residues

Total number of hits satisfying chosen parameters: 382

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 192 summaries

Database : rng.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	ADT78875	Antisense oligonuc
	2	19	95.0	20	1	ADT78876	Antisense oligonuc
	3	19	95.0	20	1	ADT78571	HIF1alpha cDNA, an
	4	18	90.0	20	1	ADT78881	Antisense oligonuc
	5	18	90.0	20	1	ADT78874	Antisense oligonuc
	6	17	85.0	20	1	ADQ88746	Human HIF-1 antise
	7	17	85.0	20	1	ADT78880	Antisense oligonuc
	8	16.8	84.0	20	1	ADT78872	Antisense oligonuc
	9	16	80.0	20	1	ADT78877	Antisense oligonuc
	10	15.8	79.0	20	1	ADT78879	Antisense oligonuc
	11	14.8	74.0	19	1	AAV13322	Sense primer Exon
	12	14	70.0	19	1	ADZ58131	Antisense siRNA ol
c	13	14	70.0	19	1	ADZ57911	Sense siRNA oligo
c	14	12.8	64.0	17	1	ABT38435	Tumour suppression
c	15	12.8	64.0	18	1	ADW14071	KCNMA1 exon 1B sen
c	16	12.2	61.0	17	1	ABN07620	Human GDMLP-1 17-m
	17	12.2	61.0	17	1	ACN12001	WNV minus strand I
c	18	12.2	61.0	17	1	ACN70710	Human GDMLP-1 prob
c	19	11.8	59.0	15	1	AAF51883	IGF-I oligonucleot
c	20	11.8	59.0	15	1	AAF51884	IGF-I oligonucleot
c	21	11.8	59.0	16	1	ADZ59539	Hyperparathyroidis
c	22	11.8	59.0	16	1	ADZ59706	Hyperparathyroidis
	23	11.4	57.0	15	1	ADG13603	Human HER1-4 hamme
c	24	11.4	57.0	16	1	ADM69289	Plant gene polymor
c	25	11.2	56.0	16	1	ADR74253	Common primer B fo
	26	11	55.0	15	1	ABK09404	Human NPR1 gene al
	27	11	55.0	15	1	ACL73850	SARS coronavirus r
	28	11	55.0	15	1	ACL73880	SARS coronavirus r
	29	11	55.0	15	1	ACL73792	SARS coronavirus r
	30	10.8	54.0	14	1	ADL96404	Acute myeloid leuk
	31	10.8	54.0	15	1	AAX31458	Tag sequence of a
c	32	10.8	54.0	15	1	AAF51885	IGF-I oligonucleot
c	33	10.8	54.0	15	1	AAF51882	IGF-I oligonucleot
	34	10.8	54.0	15	1	ABK32412	Human colon cancer
c	35	10.4	52.0	14	1	ADQ82962	Extended hairpin t
c	36	10.4	52.0	14	1	ADQ82964	Extended hairpin t
c	37	10	50.0	11	1	AED89999	Human glucose-6-ph
c	38	10	50.0	14	1	AAT36745	Antisense oligonuc
c	39	10	50.0	14	1	AAH89017	Human polymorphic
c	40	9.8	49.0	13	1	ABH45285	Oligonucleotide SE
	41	9.8	49.0	13	1	ABH45284	Oligonucleotide SE
c	42	9.8	49.0	13	1	ABH28185	Oligonucleotide SE
	43	9.8	49.0	13	1	ABH28184	Oligonucleotide SE
c	44	9.8	49.0	14	1	AAN70553	Sequence of probe
c	45	9.4	47.0	11	1	ADQ30064	Rat VR1 exon 1d tr
c	46	9.4	47.0	13	1	AAX19072	Human PPAR-gamma-3
	47	9.4	47.0	13	1	ADZ24722	Human SNP detectio
	48	9.4	47.0	13	1	AED86939	Polyamide-binding
c	49	9.4	47.0	13	1	AED86940	Polyamide-binding
	50	9	45.0	9	1	ADG13736	Human EGFR Amberzy
	51	9	45.0	10	1	ADG13703	Human EGFR Amberzy
c	52	9	45.0	11	1	AAN80414	Linker. Synthetic
c	53	9	45.0	11	1	AAZ18812	Murine C57BL/6 SAG
	54	9	45.0	11	1	ABK99449	Human CYP3A5 gene
c	55	9	45.0	12	1	AAQ88597	Human mitochondria
	56	9	45.0	12	1	AAV32269	Random primed reve
c	57	8.8	44.0	12	1	AAH23540	Antibacterial pept
	58	8.8	44.0	12	1	ABH82120	Oligonucleotide pr
	59	8.8	44.0	12	1	ABI08296	Oligonucleotide pr
	60	8.8	44.0	12	1	ADW11578	siRNA production-r
	61	8.4	42.0	10	1	AAX32635	Anticancer duplex
	62	8.4	42.0	10	1	AAX32631	Anticancer duplex
c	63	8.4	42.0	10	1	AAQ96927	HIV-1 NL4-3 nef ge
	64	8.4	42.0	10	1	AAH63224	Human colon epithe
	65	8.4	42.0	10	1	AAF38625	Yeast NORF gene SA
c	66	8.4	42.0	10	1	AAF41055	Yeast NORF gene SA
	67	8.4	42.0	10	1	AAS98404	Galanin receptor g
	68	8.4	42.0	10	1	AAD26025	Primer #27 to dete
c	69	8.4	42.0	10	1	ABK55547	Selectin L Lymphoc
	70	8.4	42.0	10	1	AAD31708	Human CD39L2 initi
	71	8.4	42.0	10	1	AAS95414	Human ICAM2 gene a
c	72	8.4	42.0	10	1	ABV84769	Chronic hepatitis
c	73	8.4	42.0	10	1	ABV84230	Human chronic hepa
	74	8.4	42.0	10	1	ABK09446	Human NPR1 gene al
	75	8.4	42.0	10	1	AAS16822	Human apolipoprote
	76	8.4	42.0	10	1	ADG98564	Human CETP gene al
	77	8.4	42.0	10	1	ADQ99469	Human CD39L2 gene
	78	8.4	42.0	10	1	ADR69198	Human CD39L2 gene
	79	8.4	42.0	10	1	ADR69032	Human CD39L2 gene
c	80	8.4	42.0	10	1	ADR87958	Cy3-labelled probe
	81	8.4	42.0	10	1	ADS17912	Human CD39L2 gene
	82	8.4	42.0	10	1	ADR87808	Human CD39L2 gene
	83	8.4	42.0	10	1	ADV16922	Human CD39L2 conse
	84	8.4	42.0	10	1	ADZ66991	Human CD39L4 RNA i
	85	8.4	42.0	10	1	ADZ74460	Human CD39L2 initi
	86	8.4	42.0	11	1	ABQ86788	Human skin stress/
	87	8.4	42.0	11	1	ABV63400	Human skin EST 118
c	88	8.4	42.0	11	1	ABV65674	Human skin EST 346
c	89	8.4	42.0	11	1	ABV64959	Human skin EST 274
	90	8.4	42.0	11	1	ABV70821	Human skin EST 860
	91	8.4	42.0	11	1	ACC58070	DNA helper probe h
	92	8.4	42.0	11	1	ACC58066	Linked nucleic aci
c	93	8.4	42.0	11	1	ADQ32820	Human facial skin-
	94	8.4	42.0	11	1	ADQ32644	Human facial skin-
c	95	8.4	42.0	11	1	ADQ32669	Human facial skin-
	96	8.4	42.0	11	1	ADZ23298	Human SNP detectio
	97	8.4	42.0	12	1	AAQ24034	Herpesvirus inhibi
c	98	8.4	42.0	12	1	AAQ30497	Adenovirus major l
c	99	8.4	42.0	12	1	AAQ52946	Herpes simplex vir
c	100	8.4	42.0	12	1	AAZ59958	Adenovirus Ad5 maj
	101	8.4	42.0	12	1	AAA30866	Fragment of a plas
c	102	8.4	42.0	12	1	ABI48155	Oligonucleotide pr
	103	8.4	42.0	12	1	ABI35107	Oligonucleotide pr
	104	8.4	42.0	12	1	ABI72389	Oligonucleotide pr
c	105	8.4	42.0	12	1	ABH84083	Oligonucleotide pr
	106	8.4	42.0	12	1	ABI04761	Oligonucleotide pr

107	8.4	42.0	12	1	ABH67680	Oligonucleotide pr
c 108	8.4	42.0	12	1	ABI08303	Oligonucleotide pr
c 109	8.4	42.0	12	1	ABI29750	Oligonucleotide pr
110	8.4	42.0	12	1	AAH49257	PNA-forming oligon
111	8.4	42.0	12	1	AAH49256	PNA-forming oligon
112	8.4	42.0	12	1	AAH49260	PNA-forming oligon
113	8.4	42.0	12	1	AAH49261	PNA-forming oligon
114	8.4	42.0	12	1	AAH49259	PNA-forming oligon
115	8.4	42.0	12	1	AAH49258	PNA-forming oligon
c 116	8.4	42.0	12	1	ABA82718	Human protective D
117	8.4	42.0	12	1	ABK72560	Human OPA1 gene, e
c 118	8.4	42.0	12	1	ABA01332	HIV-1 rev oligonuc
119	8.4	42.0	12	1	AAK98610	Modified peptide n
120	8.4	42.0	12	1	ABA97503	Peptide nucleic ac
c 121	8.4	42.0	12	1	ADM56294	Mouse SLC26A6 anio
122	8.4	42.0	12	1	ADQ29965	Rat VR1 exon 1d tr
c 123	8.4	42.0	12	1	AEF80873	MLTF/USF promoter
c 124	8	40.0	8	1	AAV63047	Synthetic RNA 8mer
125	8	40.0	8	1	AAA81073	A. thaliana primer
126	8	40.0	9	1	AAV63049	Synthetic DNA 9mer
c 127	8	40.0	9	1	AAV63048	Synthetic RNA 9mer
128	8	40.0	9	1	ADG13767	Human HER1-4 Zinzy
129	8	40.0	10	1	AAQ45113	5'-primer #24 for
130	8	40.0	10	1	AAQ96922	HIV-1 NL4-3 nef ge
131	8	40.0	10	1	AAQ96920	HIV-1 NL4-3 nef ge
132	8	40.0	10	1	AAQ96921	HIV-1 NL4-3 nef ge
133	8	40.0	10	1	AAT35724	Primer UBC556 for
c 134	8	40.0	10	1	AAT98841	Binding site BSN5-
c 135	8	40.0	10	1	AAV68349	Adapter primer oli
136	8	40.0	10	1	AAT99553	Random 10-mer prim
137	8	40.0	10	1	AAX02707	Barley HPPD primer
138	8	40.0	10	1	AAX18375	RT-PCR primer of t
139	8	40.0	10	1	AAX15555	Differential displ
140	8	40.0	10	1	AAZ77696	Human dendritic ce
141	8	40.0	10	1	AAZ79089	Human dendritic ce
142	8	40.0	10	1	AAZ84009	Metastatic breast
143	8	40.0	10	1	AAZ34693	D24 randomer used
c 144	8	40.0	10	1	AAA61006	Protein binding se
c 145	8	40.0	10	1	AAH18801	Human IL4 allele-s
c 146	8	40.0	10	1	AAF43831	Yeast NORF gene SA
c 147	8	40.0	10	1	AAF43028	Yeast NORF gene SA
148	8	40.0	10	1	ABL88465	Pain regulated gen
149	8	40.0	10	1	ABL42924	Human maturation/a
c 150	8	40.0	10	1	ABK92583	Primer-extension o
151	8	40.0	10	1	AAD45283	Human PON-1 gene p
c 152	8	40.0	10	1	ABK72438	Human HTR5A gene a
c 153	8	40.0	10	1	AAL46123	Human pro-platelet
c 154	8	40.0	10	1	ABI99138	Human PCDH2 ASO PC
c 155	8	40.0	10	1	AAL39800	SMOH polymorphism
156	8	40.0	10	1	ADD07256	Mouse differential
157	8	40.0	10	1	ADE13925	Optineurin promote
c 158	8	40.0	10	1	ADG98585	Human CETP gene al
159	8	40.0	10	1	ADL96204	CD15+ myeloid cell
160	8	40.0	10	1	ADK72504	Human pre Cinnamom
161	8	40.0	10	1	ADS76364	Breast cancer dete
162	8	40.0	11	1	ABQ87571	Human skin stress/
c 163	8	40.0	11	1	ABV67347	Human skin EST 513
164	8	40.0	11	1	ABQ78730	Nucleotide sequenc
165	8	40.0	11	1	ABA89952	ESR-alpha gene Cor
166	8	40.0	11	1	ABA89900	ESR-alpha gene Liv
167	8	40.0	11	1	ABK99375	Human CYP3A5 gene
c 168	8	40.0	11	1	ABK99363	Human CYP3A5 gene
c 169	8	40.0	11	1	ADQ30150	Murine VR1 exon 1d
170	8	40.0	11	1	ADZ23297	Human SNP detectio
171	7.8	39.0	11	1	AAX32604	Anticancer duplex
172	7.8	39.0	11	1	AAZ18893	Murine MRL SAGE ta
173	7.8	39.0	11	1	AAZ18751	Murine C57BL/6 SAG
c 174	7.8	39.0	11	1	ABV67178	Human skin EST 496
175	7.8	39.0	11	1	ABV62315	Human skin EST 101
176	7.8	39.0	11	1	ABV66218	Human skin EST 400
177	7.8	39.0	11	1	ABV64369	Human skin EST 215
178	7.8	39.0	11	1	ABV63523	Human skin EST 130
* 179	7.8	39.0	11	1	ABV66979	Human skin EST 476
180	7.8	39.0	11	1	ABV70944	Human skin EST 873
181	7.8	39.0	11	1	ABV66624	Human skin EST 441
182	7.8	39.0	11	1	ABV67607	Human skin EST 539
183	7.8	39.0	11	1	ABV71790	Human skin EST 957
c 184	7.8	39.0	11	1	ABV65780	Human skin EST 356
185	7.8	39.0	11	1	ABV69736	Human skin EST 752
c 186	7.8	39.0	11	1	ADA44629	Avian beta-defensi
187	7.8	39.0	11	1	ADK13996	Human methyl-CpG-b
c 188	7.8	39.0	11	1	ADQ35891	Human hair-bearing
189	7.8	39.0	11	1	ADQ35434	Human hair-bearing
c 190	7.8	39.0	11	1	ADQ35336	Human hair-bearing
191	7.8	39.0	11	1	ADQ34440	Human facial skin-
c 192	7.2	36.0	12	1	ADW11578	siRNA production-r

ALIGNMENTS

RESULT 1
ADT78875
ID ADT78875 standard; DNA; 20 BP.
XX
AC ADT78875;
XX
DT 27-JAN-2005 (first entry)
XX
DE Antisense oligonucleotide (ISIS 330449) for human HIF1alpha.
XX
KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS Homo sapiens.
XX
PN US2004220393-A1.
XX
PD 04-NOV-2004.
XX
PF 21-NOV-2003; 2003US-00719370.
XX
PR 23-NOV-2002; 2002US-00304126.
XX
PA (WARD/) WARD D T.
PA (DOBI/) DOBIE K W.
PA (MARC/) MARCUSSON E G.
PA (FREI/) FREIER S M.
XX
PI Ward DT, Dobie KW, Marcusson EG, Freier SM;
XX
DR WPI; 2004-774955/76.
XX
PT New antisense compound which inhibits the expression of hypoxia-inducible
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS Claim 92; SEQ ID NO 446; 195pp; English.
XX
CC The present invention relates to antisense compounds targeted to nucleic
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC comprises an antisense oligonucleotide that specifically hybridises with
CC the nucleic acid and inhibits the expression of HIF1alpha and/or
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the

```
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              ||||||||||||||||||||
Db          1 CCTCATGGTCACATGGATGA 20


RESULT 2
ADT78876
ID   ADT78876 standard; DNA; 20 BP.
XX
AC   ADT78876;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 330448) for human HIF1alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 92; SEQ ID NO 447; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACATGGATGA 20
              |||||||||||||||||||
Db          1 CTCATGGTCACATGGATGA 19


RESULT 3
ADT78571
ID   ADT78571 standard; DNA; 20 BP.
XX
AC   ADT78571;
XX
DT   27-JAN-2005  (first entry)
XX
DE   HIF1alpha cDNA, antisense oligonucleotide ISIS #298697.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; mouse; rat;
KW   phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Mus musculus.
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone. All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
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PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 27; SEQ ID NO 141; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an antisense oligonucleotide used in the
CC   examples of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              |||||||||||||||||||
Db          2 CCTCATGGTCACATGGATG 20


RESULT 4
ADT78881
ID   ADT78881 standard; DNA; 20 BP.
XX
AC   ADT78881;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 337224) for human HIF1alpha/HIF2alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   11
FT                   /*tag=  a
FT                   /mod_base= i
FT   modified_base   14
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Pseudouridine"
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Example 30; SEQ ID NO 452; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 5 G; 4 T; 0 U; 2 Other;

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              |||||||||| || ||||||
Db          1 CCTCATGGTCNCANGGATGA 20


RESULT 5
ADT78874
ID   ADT78874 standard; DNA; 20 BP.
XX
AC   ADT78874;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 330447) for human HIF1alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
```

KW hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS Homo sapiens.
XX
PN US2004220393-A1.
XX
PD 04-NOV-2004.
XX
PF 21-NOV-2003; 2003US-00719370.
XX
PR 23-NOV-2002; 2002US-00304126.
XX
PA (WARD/) WARD D T.
PA (DOBI/) DOBIE K W.
PA (MARC/) MARCUSSON E G.
PA (FREI/) FREIER S M.
XX
PI Ward DT, Dobie KW, Marcusson EG, Freier SM;
XX
DR WPI; 2004-774955/76.
XX
PT New antisense compound which inhibits the expression of hypoxia-inducible
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS Claim 92; SEQ ID NO 445; 195pp; English.
XX
CC The present invention relates to antisense compounds targeted to nucleic
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC comprises an antisense oligonucleotide that specifically hybridises with
CC the nucleic acid and inhibits the expression of HIF1alpha and/or
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC that affects the eye. The compound is also useful for treating tumours,
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC such as stenosis or restenosis following angioplasty. It is also useful
CC in drug discovery and target validation, and can be utilised for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence represents an oligonucleotide used in the examples
CC of the present invention.
XX
SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCATGGTCACATGGATGA 20
||||||||||||||||||
Db 1 TCATGGTCACATGGATGA 18

RESULT 6
ADQ88746
ID ADQ88746 standard; DNA; 20 BP.
XX
AC ADQ88746;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human HIF-1 antisense oligonucleotide RX-0041.
XX
KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;
KW cancer; infection; inflammation; tumour formation; ss;
KW antisense oligonucleotide; antisense technology; RX-0158; RX-0041.
XX
OS Homo sapiens.
XX
PN US2004152655-A1.
XX
PD 05-AUG-2004.
XX
PF 28-JAN-2004; 2004US-00766185.
XX
PR 31-JAN-2003; 2003US-0444367P.
XX
PA (YOON/) YOON H.
PA (MAOL/) MAO L.
PA (LEEY/) LEE Y B.
PA (AHNC/) AHN C.
PA (JIAN/) JIANG X.
XX
PI Yoon H, Mao L, Lee YB, Ahn C, Jiang X;
XX
DR WPI; 2004-561492/54.
XX
PT New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a
PT nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
PT useful for inhibiting expression of HIF-1 and inducing cytotoxicity in
PT several cancer cells.
XX
PS Example 4; SEQ ID NO 26; 35pp; English.
XX
CC The invention describes a compound, RX-0047 or RX-0149 targeted to a
CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
CC where the oligonucleotide compound inhibits the expression of human HIF-
CC 1. Also described are: a method of inhibiting the expression HIF-1 in
CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'
CC aatgagccaccagtgtccaa 3' and SEQ ID NO. 4, 5' ggagctaacatctccaagtc 3',
CC respectively). The compounds are useful for inhibiting the expression of
CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
CC antisense compounds are also useful for preventing or delaying infection,
CC inflammation, or tumour formation. This sequence represents a human HIF-1
CC antisense oligonucleotide.
XX
SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CATGGTCACATGGATGA 20
|||||||||||||||||
Db 1 CATGGTCACATGGATGA 17

RESULT 7
ADT78880
ID ADT78880 standard; DNA; 20 BP.
XX
AC ADT78880;
XX
DT 27-JAN-2005 (first entry)
XX
DE Antisense oligonucleotide (ISIS 337223) for human HIF1alpha/HIF2alpha.
XX
KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;

```
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   12
FT                   /*tag= a
FT                   /mod_base= i
FT   modified_base   15
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Pseudouridine"
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Example 30; SEQ ID NO 451; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 2 Other;

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 3.7;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              ||||||||||  || |||||
Db          2 CCTCATGGTCNCANGGATG 20


RESULT 8
ADT78872
ID   ADT78872 standard; DNA; 20 BP.
XX
AC   ADT78872;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 330460) for human HIF2alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 92; SEQ ID NO 443; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             84.0%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 4.1;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              ||||||||||  || ||||||
Db          1 CCTCATGGTCGCAGGGATGA 20
```

```
RESULT 9
ADT78877
ID   ADT78877 standard; DNA; 20 BP.
XX
AC   ADT78877;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 330452) for human HIF1alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 92; SEQ ID NO 448; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              ||||||||||||||||
Db          5 CCTCATGGTCACATGG 20


RESULT 10
ADT78879
ID   ADT78879 standard; DNA; 20 BP.
XX
AC   ADT78879;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 326743) for human HIF2alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 92; SEQ ID NO 450; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
```

```
  Query Match           79.0%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity  89.5%;  Pred. No. 6.4;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              ||||||||||  || |||||
Db          2 CCTCATGGTCGCAGGGATG 20


RESULT 11
AAV13322
ID   AAV13322 standard; DNA; 19 BP.
XX
AC   AAV13322;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Sense primer Exon 4 for human 5-lipoxygenase gene.
XX
KW   Inflammatory disease; polymorphism; 5-lipoxygenase; asthma;
KW   ulcerative colitis; bronchitis; sinusitis; psoriasis; rhinitis;
KW   arthritis; diagnosis; treatment; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9742347-A2.
XX
PD   13-NOV-1997.
XX
PF   29-APR-1997;   97WO-US007137.
XX
PR   06-MAY-1996;   96US-0016890P.
PR   25-APR-1997;   97US-00846020.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Drazen JM,  In K,  Asano K,  Beier D,  Grobholz J;
XX
DR   WPI; 1997-558997/51.
XX
PT   Classifying patients with inflammatory disease, specifically asthma -
PT   according to polymorphisms in 5-lipoxygenase gene regulatory region, e.g.
PT   to identify candidates for lipoxygenase inhibitor treatment.
XX
PS   Example 1; Page 19; 56pp; English.
XX
CC   The present sequence was used in the development of a novel method for
CC   classifying patients suffering from an inflammatory disease. The method
CC   comprises identifying in DNA from at least 1 patient a sequence
CC   polymorphism, as compared with the normal 5-lipoxygenase (5-LOX) gene
CC   (AAT88431), in a 5-LOX regulatory gene sequence. The method can be
CC   applied to subjects with asthma, ulcerative colitis, bronchitis,
CC   sinusitis, psoriasis, allergic and non-allergic rhinitis, lupus or
CC   rheumatoid arthritis. Specifically it can be used to diagnose asthma or
CC   susceptibility to disease, identify treatments suitable for individual
CC   patients or assess the likely success of treatment
XX
SQ   Sequence 19 BP; 4 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match           74.0%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity  88.9%;  Pred. No. 9.4;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACATGGATG 19
              ||||||  ||| |||||||
Db          2 CTCATGCTCAGATGGATG 19


RESULT 12
ADZ58131
ID   ADZ58131 standard; RNA; 19 BP.
XX
AC   ADZ58131;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Antisense siRNA oligo that modulates human HIF1 expression Seq 259.
XX
KW   ss; short interfering RNA; siRNA; gene silencing; RNA interference;
KW   hypoxia inducible factor 1; cancer; hyperproliferation;
KW   macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
KW   antidiabetic; antisense.
XX
OS   Homo sapiens.
XX
PN   WO2005035759-A2.
XX
PD   21-APR-2005.
XX
PF   20-AUG-2004; 2004WO-US027294.
XX
PR   20-AUG-2003; 2003US-0496655P.
PR   23-OCT-2003; 2003US-00693059.
PR   24-NOV-2003; 2003US-00720448.
PR   03-DEC-2003; 2003US-00727780.
PR   14-JAN-2004; 2004US-00757803.
PR   10-FEB-2004; 2004US-0543480P.
PR   13-FEB-2004; 2004US-00780447.
PR   16-APR-2004; 2004US-00826966.
PR   30-APR-2004;   54US-09997777.
PR   24-MAY-2004;   54US-09996666.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Usman N,  Mcswiggen J;
XX
DR   WPI; 2005-306364/31.
XX
PT   New chemically synthesized double stranded short interfering nucleic acid
PT   molecule that directs cleavage of a hypoxia inducible factor 1 RNA via
PT   RNA interference (RNAi), useful for modulating HIF1, its expression or
PT   activity.
XX
PS   Claim 33; SEQ ID NO 259; 189pp; English.
XX
CC   This invention relates to a novel chemically synthesized double stranded
CC   short interfering nucleic acid strand (siNA). Specifically, it refers to
CC   siNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
CC   RNA interference (RNAi). In particular, the siNAs may include short
CC   interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
CC   and short hairpin RNA (shRNA) molecules that are capable of mediating
CC   RNAi. The present invention describes a sense strand of a double-stranded
CC   siNA that comprises a nucleotide sequence that is complementary to HIF1
CC   RNA or a portion thereof, and where a second strand is the complementary
CC   antisense siNA strand. Note that the sense region is connected to the
CC   antisense region via a polynucleotide linker molecule. Accordingly, these
CC   siNAs are useful in providing compositions for the treatment of traits,
CC   diseases and conditions that respond to modulation of HIF1 expression,
CC   namely cancer and proliferative conditions including macular
CC   degeneration, diabetic retinopathy and other conditions associated with
CC   hypoxia inducible proliferation. As such, these compositions exhibit
CC   cytostatic, ophthalmological and antidiabetic activities. This
CC   oligonucleotide sequence is an antisense siRNA strand that targets human
CC   HIF1 RNA to modulate expression given in an exemplification of the
CC   invention.
XX
SQ   Sequence 19 BP; 7 A; 2 C; 6 G; 0 T; 4 U; 0 Other;

  Query Match           70.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity  78.6%;  Pred. No. 13;
  Matches   11;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGATGA 20
              ||:||||:|||:||
```

```
Db          1 GGUCACAUGGAUGA 14


RESULT 13
ADZ57911/c
ID   ADZ57911 standard; RNA; 19 BP.
XX
AC   ADZ57911;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Sense siRNA oligo that modulates human HIF1 expression Seq 39.
XX
KW   ss; short interfering RNA; siRNA; gene silencing; RNA interference;
KW   hypoxia inducible factor 1; cancer; hyperproliferation;
KW   macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
KW   antidiabetic.
XX
OS   Homo sapiens.
XX
PN   WO2005035759-A2.
XX
PD   21-APR-2005.
XX
PF   20-AUG-2004; 2004WO-US027294.
XX
PR   20-AUG-2003; 2003US-0496655P.
PR   23-OCT-2003; 2003US-00693059.
PR   24-NOV-2003; 2003US-00720448.
PR   03-DEC-2003; 2003US-00727780.
PR   14-JAN-2004; 2004US-00757803.
PR   10-FEB-2004; 2004US-0543480P.
PR   13-FEB-2004; 2004US-00780447.
PR   16-APR-2004; 2004US-00826966.
PR   30-APR-2004;   54US-09997777.
PR   24-MAY-2004;   54US-09996666.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Usman N,  Mcswiggen J;
XX
DR   WPI; 2005-306364/31.
XX
PT   New chemically synthesized double stranded short interfering nucleic acid
PT   molecule that directs cleavage of a hypoxia inducible factor 1 RNA via
PT   RNA interference (RNAi), useful for modulating HIF1, its expression or
PT   activity.
XX
PS   Claim 33; SEQ ID NO 39; 189pp; English.
XX
CC   This invention relates to a novel chemically synthesized double stranded
CC   short interfering nucleic acid strand (siNA). Specifically, it refers to
CC   siNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
CC   RNA interference (RNAi). In particular, the siNAs may include short
CC   interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
CC   and short hairpin RNA (shRNA) molecules that are capable of mediating
CC   RNAi. The present invention describes a sense strand of a double-stranded
CC   siNA that comprises a nucleotide sequence that is complementary to HIF1
CC   RNA or a portion thereof, and where a second strand is the complementary
CC   antisense siNA strand. Note that the sense region is connected to the
CC   antisense region via a polynucleotide linker molecule. Accordingly, these
CC   siNAs are useful in providing compositions for the treatment of traits,
CC   diseases and conditions that respond to modulation of HIF1 expression,
CC   namely cancer and proliferative conditions including macular
CC   degeneration, diabetic retinopathy and other conditions associated with
CC   hypoxia inducible proliferation. As such, these compositions exhibit
CC   cytostatic, ophthalmological and antidiabetic activities. This
CC   oligonucleotide sequence is a sense siRNA strand that targets human HIF1
CC   RNA to modulate expression given in an exemplification of the invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

  Query Match           70.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGATGA 20
              ||||||||||||||
Db         19 GGTCACATGGATGA 6


RESULT 14
ABT38435/c
ID   ABT38435 standard; DNA; 17 BP.
XX
AC   ABT38435;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Tumour suppression related human fukutin oligo SEQ ID No 4072.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW   antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW   schizophrenia; protein chip; gene therapy; tumour suppression;
KW   human fukutin; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003025175-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004208.
XX
PR   17-SEP-2001; 2001FR-00011978.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-313353/30.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; Page 510; 720pp; French.
XX
CC   The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC   given in the specification, a sequence containing at least 15 consecutive
CC   nucleotides from the 17 mer sequence, a sequence with, after optimal
CC   alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC   hybridizes to them under highly stringent conditions, or the complement
CC   of any of them, or the corresponding RNA. The novel isolated nucleic
CC   acids of the invention are useful as probes and primers for detecting,
CC   identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC   component of a gene chip, in vitro as (anti)sense reagents, and for
CC   production of recombinant polypeptides. Any of the nucleic acids,
CC   polypeptides, vectors containing the nucleic acids, cells containing the
CC   vector or antibodies directed against the polypeptides are useful for
CC   preparation of pharmaceuticals for prevention and/or treatment of viral
CC   diseases that are characterised by development of tumours or cell
CC   degeneration, specifically cancer but also Alzheimer's disease and
CC   schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC   patient samples is useful for diagnosis and/or prognosis of these
CC   diseases. The polypeptides can also be used to generate antibodies, and
CC   both the polypeptide and antibodies are useful as components of protein
CC   chips. The nucleic acid sequences of the invention can be used in gene
CC   therapy. This polynucleotide sequence represents a tumour suppression
CC   related human fukutin oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 4 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match           64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity  87.5%;  Pred. No. 20;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          3 TCATGGTCACATGGAT 18
              ||| ||||| ||||||
Db         17 TCAAGGTCAAATGGAT 2
```

RESULT 15
ADW14071/c
ID ADW14071 standard; DNA; 18 BP.
XX
AC ADW14071;
XX
DT 07-APR-2005 (first entry)
XX
DE KCNMA1 exon 1B sense PCR primer, SEQ ID 3.
XX
KW Nootropic; autism; potassium channel; KCNMA1; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN FR2857452-A1.
XX
PD 14-JAN-2005.
XX
PF 11-JUL-2003; 2003FR-00008527.
XX
PR 11-JUL-2003; 2003FR-00008527.
XX
PA (UYRA-) UNIV RABELAIS FRANCOIS.
XX
PI Briault S, Laumonnier F, Le Guennec JY, Roger S;
XX
DR WPI; 2005-114499/13.
XX
PT Test for identifying autism, comprises detecting reduction in activity of
PT calcium-dependent potassium channels by measuring the electrical activity
PT of the channels.
XX
PS Example 1; SEQ ID NO 3; 42pp; French.
XX
CC The present invention relates to a test for detecting autism, which
CC comprises measuring the electrical activity of calcium-dependent
CC potassium channels (BKCa) in a sample of blood cells and detecting any
CC reduction in activity, relative to a control sample. Also claimed are:
CC selecting a subpopulation of patients with autism by performing the new
CC method and selecting subjects with reduced BKCa activity; and use of
CC activators or agonists of BKCa to prepare a composition for treating
CC autism where this is associated with deficient electrical activity. The
CC method is useful for autism diagnosis and prognosis and to identify a
CC subset of autism patients who may benefit from treatment with activators
CC or agonists (X) of BKCa, i.e. patients where autism is linked to a
CC defective electrical activity. In an example from the invention, a
CC translocation in the potassium channel KCNMA1 gene in a six year old
CC patient with autism was detected and characterized using PCR primers
CC ADW14069-ADW14128. The KCNMA1 gene encodes a protein of the glutaminergic
CC complex, and mutation of the KCNMA1 gene resulting in inadequate
CC functioning of BKCa. The translocation was [46, XY, t(9;10) (q23;q22)],
CC and the break was between the first and second exons of the KCNMA1 gene
CC and amplification tests showed that, in the patient, one copy of the
CC KCNMA1 was inactivated.
XX
SQ Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match   64.0%; Score 12.8; DB 1; Length 18;
  Best Local Similarity   87.5%; Pred. No. 21;
  Matches   14; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

```
Qy          4 CATGGTCACATGGATG 19
              |||||||||  |||||
Db         16 CATGGTCACCGGGATG 1
```

RESULT 16
ABN07620/c
ID ABN07620 standard; DNA; 17 BP.
XX
AC ABN07620;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7612.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 7612; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

```
  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 26;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 17
ACN12001
ID   ACN12001 standard; RNA; 17 BP.
XX
AC   ACN12001;
XX
DT   22-APR-2004  (first entry)
XX
DE   WNV minus strand Inozyme substrate SEQ ID NO 12004.
XX
KW   WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW   virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW   encephalitis; myocarditis; meningitis; infection; hepatitis;
KW   liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW   Amberzyme; Zinzyme; ss.
XX
OS   West Nile Virus.
XX
PN   WO200268637-A2.
XX
PD   06-SEP-2002.
XX
PF   19-OCT-2001; 2001WO-US048350.
XX
PR   20-OCT-2000; 2000US-0242411P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
XX
PI   Blatt L,  Mcswiggen JA;
XX
DR   WPI; 2002-706994/76.
XX
PT   New nucleic acid molecule that modulates replication of West Nile Virus
PT   (WNV), useful for treating a condition related to WNV infection e.g.
PT   pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS   Claim 23; SEQ ID NO 12004; 495pp; English.
XX
CC   The invention relates to nucleic acid molecules that modulate replication
CC   of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC   treating a condition related to WNV infection e.g. pancreatitis,
CC   encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC   liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC   molecule is selected from the group of ribozymes consisting of
CC   Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC   nucleic acid molecules further comprise at least five ribose residues, at
CC   least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC   least three of the 5' terminal nucleotides and a 3' end modification of a
CC   3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC   are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC   in the specification. The present sequence is that of a nucleic acid
CC   molecule of the invention
XX
SQ   Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   52.9%;  Pred. No. 26;
  Matches    9;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATG 19
              :||:  :||||: ||:|
Db          1 UCAUCUUCACAUCGAUG 17


RESULT 18
ACN70710/c
ID   ACN70710 standard; DNA; 17 BP.
XX
AC   ACN70710;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human GDMLP-1 probe SEQ ID NO:7612.
XX
KW   Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW   hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW   skeletal muscle function.
XX
OS   Homo sapiens.
XX
PN   US2004137589-A1.
XX
PD   15-JUL-2004.
XX
PF   26-NOV-2003; 2003US-00723361.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
PR   25-MAY-2001; 2001US-00866108.
XX
PA   (GUYY/) GU Y.
PA   (JIYY/) JI Y.
PA   (PENN/) PENN S G.
PA   (HANZ/) HANZEL D K.
PA   (RANK/) RANK D.
PA   (CHEN/) CHEN W.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank D,  Chen W,  Shannon ME;
XX
DR   WPI; 2004-533378/51.
XX
PT   Novel myosin-like protein-1, useful for treating or preventing disorder
PT   associated with decreased expression or activity of human genome-derived
PT   myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT   function.
XX
PS   Disclosure; SEQ ID NO 7612; 0pp; English.
XX
CC   The invention relates to a novel polypeptide (I) comprising a sequence
CC   (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC   defined in the specification, a fragment of at least 8 amino acids of
CC   (S1), 95% deviation from (S1) which are conservative substitutions, and
CC   65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC   antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC   pharmaceutical composition of the invention is useful for treating or
CC   preventing a disorder associated with decreased expression or activity of
CC   hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC   The present sequence represents a 17-mer nucleotide, used in the
CC   invention for scanning the sequence represented in ACN63103
XX
```

```
SQ   Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match           61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity  82.4%;  Pred. No. 26;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 19
AAF51883/c
ID   AAF51883 standard; DNA; 15 BP.
XX
AC   AAF51883;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2843.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 79; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match           59.0%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity  86.7%;  Pred. No. 26;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              || ||| |||||||
Db         15 TGATCAGATGGATGA 1


RESULT 20
AAF51884/c
ID   AAF51884 standard; DNA; 15 BP.
XX
AC   AAF51884;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2844.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 79; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match           59.0%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity  86.7%;  Pred. No. 26;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGATG 19
              ||| ||| |||||||
```

```
Db         15 ATGATCAGATGGATG 1


RESULT 21
ADZ59539/c
ID   ADZ59539 standard; DNA; 16 BP.
XX
AC   ADZ59539;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Hyperparathyroidism polymorphic detection VIC probe, SEQ ID 33.
XX
KW   secondary hyperparathyroidism; endocrine-gen.; antithyroid;
KW   renal failure; nephrotropic; SNP detection; ss; probe.
XX
OS   Synthetic.
XX
PN   JP2005102601-A.
XX
PD   21-APR-2005.
XX
PF   30-SEP-2003; 2003JP-00341015.
XX
PR   30-SEP-2003; 2003JP-00341015.
XX
PA   (HYUB-) HYUBITTO GENOMICS KK.
PA   (JIKE-) UNIV JIKEI.
XX
DR   WPI; 2005-358641/37.
XX
PT   Testing secondary hyperparathyroidism in chronic renal failure patient,
PT   involves detecting variation in gene chosen from CACNA1C, CALCRL, CHI3L1,
PT   EGF, FGF1, GFRA1, GPR56 and GPRK6.
XX
PS   Disclosure; SEQ ID NO 33; 138pp; Japanese.
XX
CC   The invention relates to a novel method for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. The method
CC   involves detecting a variation in a gene chosen from CACNA1C, CALCRL,
CC   CHI3L1, EGF, FGF1, GFRA1, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNJ14,
CC   KCNQ1, ORCTL4, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,
CC   IL17R, OSTF1, FGF6, HGF, MET, TGFB1 and VEGF, or detecting the base in a
CC   polymorphism region existing in the vicinity of any one of the genes. The
CC   invention further comprises a reagent or kit for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. This
CC   polynucleotide sequence represents a probe used in the detection of a
CC   polymorphism in a gene linked to secondary hyperparathyroidism of the
CC   invention.
XX
SQ   Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 28;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGA 17
              || |||||||| |||
Db         16 TCTTGGTCACAGGGA 2


RESULT 22
ADZ59706/c
ID   ADZ59706 standard; DNA; 16 BP.
XX
AC   ADZ59706;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Hyperparathyroidism polymorphic detection VIC probe, SEQ ID 200.
XX
KW   secondary hyperparathyroidism; endocrine-gen.; antithyroid;
KW   renal failure; nephrotropic; SNP detection; ss; probe.
XX
OS   Synthetic.
XX
PN   JP2005102601-A.
XX
PD   21-APR-2005.
XX
PF   30-SEP-2003; 2003JP-00341015.
XX
PR   30-SEP-2003; 2003JP-00341015.
XX
PA   (HYUB-) HYUBITTO GENOMICS KK.
PA   (JIKE-) UNIV JIKEI.
XX
DR   WPI; 2005-358641/37.
XX
PT   Testing secondary hyperparathyroidism in chronic renal failure patient,
PT   involves detecting variation in gene chosen from CACNA1C, CALCRL, CHI3L1,
PT   EGF, FGF1, GFRA1, GPR56 and GPRK6.
XX
PS   Disclosure; SEQ ID NO 200; 138pp; Japanese.
XX
CC   The invention relates to a novel method for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. The method
CC   involves detecting a variation in a gene chosen from CACNA1C, CALCRL,
CC   CHI3L1, EGF, FGF1, GFRA1, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNJ14,
CC   KCNQ1, ORCTL4, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,
CC   IL17R, OSTF1, FGF6, HGF, MET, TGFB1 and VEGF, or detecting the base in a
CC   polymorphism region existing in the vicinity of any one of the genes. The
CC   invention further comprises a reagent or kit for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. This
CC   polynucleotide sequence represents a probe used in the detection of a
CC   polymorphism in a gene linked to secondary hyperparathyroidism of the
CC   invention.
XX
SQ   Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 28;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGA 17
              || |||||||| |||
Db         16 TCTTGGTCACAGGGA 2


RESULT 23
ADG13603
ID   ADG13603 standard; RNA; 15 BP.
XX
AC   ADG13603;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human HER1-4 hammerhead ribozyme target sequence #3.
XX
KW   Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
KW   HER4; hammerhead ribozyme; inozyme; zinzyme; DNAzyme; amberzyme; cancer;
KW   brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;
KW   prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW   stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW   head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW   multidrug resistant cancer.
XX
OS   Homo sapiens.
XX
PN   US2003186909-A1.
XX
PD   02-OCT-2003.
XX
PF   21-OCT-2002; 2002US-00277494.
XX
PR   27-JAN-1997;   97US-0036749P.
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PR   04-DEC-1997;   97US-00985162.
PR   22-SEP-1999;   99US-00401063.
PR   03-MAY-2001; 2001US-00848754.
PR   25-JUL-2001; 2001US-00916466.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2004-032029/03.
XX
PT   New double stranded short interfering ribonucleic acid molecule for
PT   inhibiting expression of epidermal growth factor receptor gene.
XX
PS   Claim 7; SEQ ID NO 30; 113pp; English.
XX
CC   The invention relates to a double stranded short interfering RNA (siRNA)
CC   molecule that inhibits expression of epidermal growth factor receptor
CC   (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
CC   expression vector comprising a nucleic acid sequence encoding siRNA
CC   molecule(s) in a manner that allows expression of the nucleic acid
CC   molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
CC   amberzymes zinzymes and DNAzymes. The invention is used for inhibiting
CC   expression of EGFR. It can be used for treatment of cancer, prostate
CC   cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC   cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC   cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC   cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC   life in vitro , stability, and ease of introduction of oligonucleotide to
CC   target site. The present sequence is an EGFR/HER1-4 target sequence for
CC   an siRNA of the invention.
XX
SQ   Sequence 15 BP; 4 A; 2 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 30;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              :||:||:|| |:|
Db          1 UCAUGGUCAAAUG 13


RESULT 24
ADM69289/c
ID   ADM69289 standard; DNA; 16 BP.
XX
AC   ADM69289;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Plant gene polymorphism marker related primer, SEQ ID 168.
XX
KW   Primer; variation mapping; mutation mapping; plant;
KW   gene polymorphism marker; ss.
XX
OS   Synthetic.
XX
PN   JP2003289885-A.
XX
PD   14-OCT-2003.
XX
PF   31-JAN-2003; 2003JP-00024620.
XX
PR   01-FEB-2002; 2002JP-00025338.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (SAIM-) SAI MEDIA KK.
PA   (MATS/) MATSUI M.
PA   (NAKA/) NAKAZAWA M.
XX
DR   WPI; 2004-126231/13.
XX
PT   A primer set and method useful for mapping at least the
PT   variation/mutation part of a plant gene using a gene polymorphism marker.
XX
PS   Claim 7; SEQ ID NO 168; 120pp; Japanese.
XX
CC   The present invention relates to a primer set and method for mapping at
CC   least the variation/mutation part of a plant gene using a gene
CC   polymorphism marker. A mutation site of the plant gene is mapped by
CC   utilizing a genetic polymorphism marker as follows: (a) genomic DNA is
CC   prepared from a plant homozygously having a mutation to be an object of
CC   the mapping; (b) A forward primer 1 containing a base corresponding to
CC   the gene polymorphic maker of one ecotype plant, a forward primer 2
CC   containing a base corresponding to the genetic polymorphism of the other
CC   ecotype plant and a reverse primer 3 based on the base sequence common
CC   with both the ecotype plants are prepared; (c) two kinds of
CC   oligonucleotides emitting fluorescence of different colors when the
CC   genetic polymorphism marker is detected are prepared; (d) an
CC   amplification reaction of the genomic DNA is carried out in the presence
CC   of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
CC   the fluorescence intensity emitted from the resultant reactional product
CC   is detected and (f) the position on the genome of the mutation site is
CC   determined from the results of detection. The present sequence is a
CC   primer, used to illustrate the invention.
XX
SQ   Sequence 16 BP; 2 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 16;
  Best Local Similarity   92.3%;  Pred. No. 33;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              |||||||||| ||
Db         14 GTCACATGGAGGA 2


RESULT 25
ADR74253/c
ID   ADR74253 standard; DNA; 16 BP.
XX
AC   ADR74253;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Common primer B for human MI-associated marker hCV2633049.
XX
KW   Human; ss; PCR; primer; SNP; single nucleotide polymorphism;
KW   myocardial infarction.
XX
OS   Homo sapiens.
XX
PN   WO2004081187-A2.
XX
PD   23-SEP-2004.
XX
PF   10-MAR-2004; 2004WO-US007141.
XX
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O,  Shiffman D;
XX
DR   WPI; 2004-677537/66.
XX
PT   Identifying an individual who has altered risk for developing myocardial
PT   infarction comprises detecting single nucleotide polymorphism (SNP), in
PT   the individual's nucleic acids.
XX
PS   Claim 19; SEQ ID NO 44078; 139pp; English.
XX
CC   The invention relates to identifying an individual who has altered risk
CC   for developing myocardial infarction comprises detecting single
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CC   nucleotide polymorphism (SNP) in any one of the 43336 nucleotide
CC   sequences (not given in the specification), in the individual's nucleic
CC   acids, where the presence of the SNP is correlated with an altered risk
CC   for myocardial infarction in the individual. Also included are an
CC   isolated nucleic acid molecule (comprising at least 8 contiguous
CC   nucleotides where one of the nucleotides is an SNP as cited above, or
CC   their complement), an isolated polypeptide comprising an amino acid
CC   sequence selected from any of the 696 amino acid sequences not defined in
CC   the specification, an antibody that specifically binds to the polypeptide
CC   (or its antigen-binding fragment), an amplified polynucleotide containing
CC   the SNP as cited (where the amplified polynucleotide is between about 16
CC   and about 1,000 nucleotides in length), an isolated polynucleotide which
CC   specifically hybridises to a nucleic acid molecule containing the SNP, a
CC   kit for detecting SNP in a nucleic acid, detecting SNP in a nucleic acid
CC   molecule, detecting a variant polypeptide and identifying an agent useful
CC   in therapeutically or prophylactically treating myocardial infarction.
CC   The detection step of the method is carried out by a process selected
CC   from allele-specific probe hybridisation, allele-specific primer
CC   extension, allele-specific amplification, sequencing, 5' nuclease
CC   digestion, molecular beacon assay, oligonucleotide ligation assay, size
CC   analysis, and single-stranded conformation polymorphism. The method is
CC   useful for identifying an individual who has altered risk for developing
CC   myocardial infarction. The present sequence is common primer (used with
CC   an allele specific PCR primer) used to amplify an SNP-containing region
CC   from a myocardial infarction-associated marker gene. NOTE: SEQ IDs 1-
CC   43787 are not shown in the specification and are not available from WIPO.
CC   These sequence are contained on a CD-R named CL001509CDR which has not
CC   been supplied with the specification.
XX
SQ   Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             56.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 36;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              | |||||| ||| |||
Db         16 CTTCATGGGCACGTGG 1


RESULT 26
ABK09404
ID   ABK09404 standard; DNA; 15 BP.
XX
AC   ABK09404;
XX
DT   14-MAR-2002  (first entry)
XX
DE   Human NPR1 gene allele-specific oligonucleotide sequencing primer #26.
XX
KW   Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; ss;
KW   atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
KW   haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
KW   drug screening; hypertension; hypotensive; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200179231-A2.
XX
PD   25-OCT-2001.
XX
PF   16-APR-2001; 2001WO-US012300.
XX
PR   14-APR-2000; 2000US-0197330P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Choi JY,  Kliem SE,  Nandabalan K;
XX
DR   WPI; 2002-066340/09.
XX
PT   Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of
PT   an individual, involves determining identity of nucleotide pair at
PT   specific polymorphic sites for two copies of the gene.
XX
PS   Claim 15; Page 14; 96pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding the human natriuretic peptide receptor A/guanylate cyclase A
CC   (atrionatriuretic peptide receptor A) or NPR1 polypeptide. A method for
CC   haplotyping the NPR1 gene in an individual comprises identifying the
CC   nucleotide at one or more polymorphic sites and determining whether one
CC   of the copies of the gene is defined by one of the NPR1 haplotypes given
CC   in the specification or whether both copies are defined by a haplotype
CC   pair. This method is useful in genotyping, whereby all possible haplotype
CC   pairs can be assigned to specific genotypes. An association between a
CC   trait and a haplotype or haplotype pair of the NPR1 gene can be
CC   identified by comparing the frequency of the haplotype or haplotype pair
CC   in a population exhibiting the trait with the frequency of the haplotype
CC   or haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. NPR1 and its corresponding DNA are used
CC   for studying the expression and function of NPR1, for use in screening
CC   for candidate drugs to treat diseases related to NPR1 activity, such as
CC   hypertension. The sequences are also useful for studying the effect of
CC   variation on the biological activity of NPR1 as well as on the binding
CC   affinity of candidate drugs targeting NPR1. Sequences AAS99959-AAS99990
CC   and ABK09390-ABK09462 represent probes, sequencing primers and PCR
CC   primers used to detect NPR1 gene polymorphisms
XX
SQ   Sequence 15 BP; 5 A; 4 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 36;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACAT 14
              |||| |||||||:
Db          2 CTCAAGGTCACAY 14


RESULT 27
ACL73850
ID   ACL73850 standard; DNA; 15 BP.
XX
AC   ACL73850;
XX
DT   16-JUN-2005  (first entry)
XX
DE   SARS coronavirus right PCR primer, SEQ:631.
XX
KW   Vaccine; nucleic acid vaccine; drug screening; diagnosis;
KW   SARS coronavirus infection; infection; respiratory disease; virucide;
KW   PCR; primer; ss.
XX
OS   SARS coronavirus.
XX
PN   WO2004092360-A2.
XX
PD   28-OCT-2004.
XX
PF   09-APR-2004; 2004WO-US011710.
XX
PR   10-APR-2003; 2003US-0462218P.
PR   11-APR-2003; 2003US-0462465P.
PR   12-APR-2003; 2003US-0462418P.
PR   13-APR-2003; 2003US-0462748P.
PR   14-APR-2003; 2003US-0463109P.
PR   15-APR-2003; 2003US-0463460P.
PR   16-APR-2003; 2003US-0463668P.
PR   17-APR-2003; 2003US-0463983P.
PR   18-APR-2003; 2003US-0463971P.
PR   22-APR-2003; 2003US-0464838P.
PR   22-APR-2003; 2003US-0464899P.
PR   23-APR-2003; 2003US-0465273P.
PR   24-APR-2003; 2003US-0465535P.
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PR   05-MAY-2003; 2003US-0468312P.
PR   22-MAY-2003; 2003US-0473144P.
PR   14-AUG-2003; 2003US-0495024P.
PR   23-SEP-2003; 2003US-0505652P.
PR   11-OCT-2003; 2003US-0510781P.
PR   11-DEC-2003; 2003US-0529464P.
PR   12-JAN-2004; 2004US-0536177P.
PR   07-APR-2004; 2004US-0560757P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;
PI   Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JJ;
PI   Klenk HD, Valiante N;
XX
DR   WPI; 2004-766863/75.
XX
PT   Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
PT   severe acute respiratory syndrome virus (SARS), useful as vaccine for
PT   SARS.
XX
PS   Claim 59; SEQ ID NO 631; 839pp; English.
XX
CC   The invention relates to isolated polypeptides of the severe acute
CC   respiratory syndrome (SARS) coronavirus. The polypeptides include spike
CC   (S or E2), env (E or sM), membrane (M or E1), hemagglutinin-esterase (HE
CC   or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
CC   (replicase) polypeptides and their proteolytic fragments. The invention
CC   also relates to antibodies which recognise the polypeptides; nucleic
CC   acids encoding the SARS virus polypeptides; primers specific for SARS
CC   virus nucleic acid sequences; kits for amplifying SARS virus target
CC   nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
CC   which is able to inactivate the SARS virus in a mammalian cell; an
CC   expression construct for recombinant expression of a SARS virus spike
CC   protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
CC   encoding nucleic acid; and a mammalian cell line stably expressing a SARS
CC   viral antigen. The invention additionally provides a vaccine for the
CC   treatment or prevention of SARS comprising an inactivated SARS virus, a
CC   killed SARS virus, an attenuated SARS virus, a split SARS virus
CC   preparation, or at least one purified SARS virus antigens; methods of
CC   making inactivated SARS virus and vaccines containing it; an alpha-virus
CC   replicon particle comprising one or more SARS viral antigens; and a
CC   vaccine comprising one or more SARS virus antigens and one or more
CC   respiratory virus antigens. The invention further encompasses a method of
CC   identifying a therapeutically active agent by measuring the effect of the
CC   agent on a SARS-related enzyme, and a method of treating a SARS patient
CC   using small molecule viral inhibitors. The SARS virus polypeptides and
CC   nucleic acids can be used in the preparation and manufacture of vaccines
CC   for the treatment or prevention of SARS. The SARS virus polypeptides,
CC   antibodies against them, and SARS virus-specific primers and kits
CC   containing them are useful for diagnosing or identifying the presence of
CC   SARS in a biological sample. The present sequence represents a PCR primer
CC   for amplifying a SARS coronavirus gene. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||||||||||
Db          5 CTCATGGTCAC 15


RESULT 28
ACL73880
ID   ACL73880 standard; DNA; 15 BP.
XX
AC   ACL73880;
XX
DT   16-JUN-2005  (first entry)
XX
DE   SARS coronavirus right PCR primer, SEQ:661.
XX
KW   Vaccine; nucleic acid vaccine; drug screening; diagnosis;
KW   SARS coronavirus infection; infection; respiratory disease; virucide;
KW   PCR; primer; ss.
XX
OS   SARS coronavirus.
XX
PN   WO2004092360-A2.
XX
PD   28-OCT-2004.
XX
PF   09-APR-2004; 2004WO-US011710.
XX
PR   10-APR-2003; 2003US-0462218P.
PR   11-APR-2003; 2003US-0462465P.
PR   12-APR-2003; 2003US-0462418P.
PR   13-APR-2003; 2003US-0462748P.
PR   14-APR-2003; 2003US-0463109P.
PR   15-APR-2003; 2003US-0463460P.
PR   16-APR-2003; 2003US-0463668P.
PR   17-APR-2003; 2003US-0463983P.
PR   18-APR-2003; 2003US-0463971P.
PR   22-APR-2003; 2003US-0464838P.
PR   22-APR-2003; 2003US-0464899P.
PR   23-APR-2003; 2003US-0465273P.
PR   24-APR-2003; 2003US-0465535P.
PR   05-MAY-2003; 2003US-0468312P.
PR   22-MAY-2003; 2003US-0473144P.
PR   14-AUG-2003; 2003US-0495024P.
PR   23-SEP-2003; 2003US-0505652P.
PR   11-OCT-2003; 2003US-0510781P.
PR   11-DEC-2003; 2003US-0529464P.
PR   12-JAN-2004; 2004US-0536177P.
PR   07-APR-2004; 2004US-0560757P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;
PI   Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JJ;
PI   Klenk HD, Valiante N;
XX
DR   WPI; 2004-766863/75.
XX
PT   Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
PT   severe acute respiratory syndrome virus (SARS), useful as vaccine for
PT   SARS.
XX
PS   Claim 59; SEQ ID NO 661; 839pp; English.
XX
CC   The invention relates to isolated polypeptides of the severe acute
CC   respiratory syndrome (SARS) coronavirus. The polypeptides include spike
CC   (S or E2), env (E or sM), membrane (M or E1), hemagglutinin-esterase (HE
CC   or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
CC   (replicase) polypeptides and their proteolytic fragments. The invention
CC   also relates to antibodies which recognise the polypeptides; nucleic
CC   acids encoding the SARS virus polypeptides; primers specific for SARS
CC   virus nucleic acid sequences; kits for amplifying SARS virus target
CC   nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
CC   which is able to inactivate the SARS virus in a mammalian cell; an
CC   expression construct for recombinant expression of a SARS virus spike
CC   protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
CC   encoding nucleic acid; and a mammalian cell line stably expressing a SARS
CC   viral antigen. The invention additionally provides a vaccine for the
CC   treatment or prevention of SARS comprising an inactivated SARS virus, a
CC   killed SARS virus, an attenuated SARS virus, a split SARS virus
CC   preparation, or at least one purified SARS virus antigens; methods of
CC   making inactivated SARS virus and vaccines containing it; an alpha-virus
CC   replicon particle comprising one or more SARS viral antigens; and a
CC   vaccine comprising one or more SARS virus antigens and one or more
```

```
CC   respiratory virus antigens. The invention further encompasses a method of
CC   identifying a therapeutically active agent by measuring the effect of the
CC   agent on a SARS-related enzyme, and a method of treating a SARS patient
CC   using small molecule viral inhibitors. The SARS virus polypeptides and
CC   nucleic acids can be used in the preparation and manufacture of vaccines
CC   for the treatment or prevention of SARS. The SARS virus polypeptides,
CC   antibodies against them, and SARS virus-specific primers and kits
CC   containing them are useful for diagnosing or identifying the presence of
CC   SARS in a biological sample. The present sequence represents a PCR primer
CC   for amplifying a SARS coronavirus gene. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||||||||||
Db          1 CTCATGGTCAC 11


RESULT 29
ACL73792
ID   ACL73792 standard; DNA; 15 BP.
XX
AC   ACL73792;
XX
DT   16-JUN-2005  (first entry)
XX
DE   SARS coronavirus right PCR primer, SEQ:573.
XX
KW   Vaccine; nucleic acid vaccine; drug screening; diagnosis;
KW   SARS coronavirus infection; infection; respiratory disease; virucide;
KW   PCR; primer; ss.
XX
OS   SARS coronavirus.
XX
PN   WO2004092360-A2.
XX
PD   28-OCT-2004.
XX
PF   09-APR-2004; 2004WO-US011710.
XX
PR   10-APR-2003; 2003US-0462218P.
PR   11-APR-2003; 2003US-0462465P.
PR   12-APR-2003; 2003US-0462418P.
PR   13-APR-2003; 2003US-0462748P.
PR   14-APR-2003; 2003US-0463109P.
PR   15-APR-2003; 2003US-0463460P.
PR   16-APR-2003; 2003US-0463668P.
PR   17-APR-2003; 2003US-0463983P.
PR   18-APR-2003; 2003US-0463971P.
PR   22-APR-2003; 2003US-0464838P.
PR   22-APR-2003; 2003US-0464899P.
PR   23-APR-2003; 2003US-0465273P.
PR   24-APR-2003; 2003US-0465535P.
PR   05-MAY-2003; 2003US-0468312P.
PR   22-MAY-2003; 2003US-0473144P.
PR   14-AUG-2003; 2003US-0495024P.
PR   23-SEP-2003; 2003US-0505652P.
PR   11-OCT-2003; 2003US-0510781P.
PR   11-DEC-2003; 2003US-0529464P.
PR   12-JAN-2004; 2004US-0536177P.
PR   07-APR-2004; 2004US-0560757P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Rappuoli R,  Masignani V,  Stadler K,  Gregersen J,  Chien D,  Han J;
PI   Polo J,  Weiner A,  Houghton M,  Song HC,  Seo MY,  Donnelly JJ;
PI   Klenk HD,  Valiante N;
XX
DR   WPI; 2004-766863/75.
XX
PT   Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
PT   severe acute respiratory syndrome virus (SARS), useful as vaccine for
PT   SARS.
XX
PS   Claim 59; SEQ ID NO 573; 839pp; English.
XX
CC   The invention relates to isolated polypeptides of the severe acute
CC   respiratory syndrome (SARS) coronavirus. The polypeptides include spike
CC   (S or E2), env (E or sM), membrane (M or E1), hemagglutinin-esterase (HE
CC   or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
CC   (replicase) polypeptides and their proteolytic fragments. The invention
CC   also relates to antibodies which recognise the polypeptides; nucleic
CC   acids encoding the SARS virus polypeptides; primers specific for SARS
CC   virus nucleic acid sequences; kits for amplifying SARS virus target
CC   nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
CC   which is able to inactivate the SARS virus in a mammalian cell; an
CC   expression construct for recombinant expression of a SARS virus spike
CC   protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
CC   encoding nucleic acid; and a mammalian cell line stably expressing a SARS
CC   viral antigen. The invention additionally provides a vaccine for the
CC   treatment or prevention of SARS comprising an inactivated SARS virus, a
CC   killed SARS virus, an attenuated SARS virus, a split SARS virus
CC   preparation, or at least one purified SARS virus antigens; methods of
CC   making inactivated SARS virus and vaccines containing it; an alpha-virus
CC   replicon particle comprising one or more SARS viral antigens; and a
CC   vaccine comprising one or more SARS virus antigens and one or more
CC   respiratory virus antigens. The invention further encompasses a method of
CC   identifying a therapeutically active agent by measuring the effect of the
CC   agent on a SARS-related enzyme, and a method of treating a SARS patient
CC   using small molecule viral inhibitors. The SARS virus polypeptides and
CC   nucleic acids can be used in the preparation and manufacture of vaccines
CC   for the treatment or prevention of SARS. The SARS virus polypeptides,
CC   antibodies against them, and SARS virus-specific primers and kits
CC   containing them are useful for diagnosing or identifying the presence of
CC   SARS in a biological sample. The present sequence represents a PCR primer
CC   for amplifying a SARS coronavirus gene. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||||||||||
Db          4 CTCATGGTCAC 14


RESULT 30
ADL96404
ID   ADL96404 standard; DNA; 14 BP.
XX
AC   ADL96404;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Acute myeloid leukaemia (AML) associated EST seqid 303.
XX
KW   cytostatic; gene therapy; microarray; gene expression characteristic;
KW   haematopoietic cell; haematopoiesis; myeloid leukaemia; EST;
KW   expressed sequence tag; acute myeloid leukaemia; AML; translocation; t(9;
KW   11); ss.
XX
OS   Homo sapiens.
XX
PN   US2003165949-A1.
```

```
XX
PD   04-SEP-2003.
XX
PF   23-DEC-2002; 2002US-00329465.
XX
PR   27-DEC-2001; 2001US-0343826P.
XX
PA   (WANG/) WANG S M.
PA   (LEES/) LEE S.
PA   (CHEN/) CHEN J.
PA   (ZHOU/) ZHOU G.
PA   (ROWL/) ROWLEY J D.
XX
PI   Wang SM,  Lee S,  Chen J,  Zhou G,  Rowley JD;
XX
DR   WPI; 2003-863699/80.
XX
PT   New microarray for measuring gene expression characteristics of
PT   hematopoietic cells, useful for preparing a composition for diagnosing or
PT   treating myeloid leukemia.
XX
PS   Example 3; SEQ ID NO 303; 32pp; English.
XX
CC   The invention describes a microarray for measuring gene expression
CC   characteristics of haematopoietic cells comprising at least 5
CC   polynucleotides having distinct sequences. Also described are: a method
CC   of diagnosing or treating an abnormality associated with haematopoiesis;
CC   and diagnosing myeloid leukaemia in a patient. The microarray is useful
CC   for preparing a composition for diagnosing or treating myeloid leukaemia.
CC   This sequence represents an expressed sequence tag (EST) isolated from a
CC   cell of a patient with acute myeloid leukaemia with the t(9;11)
CC   translocation that results in the mixed-lineage leukaemia (MML)-AF9
CC   fusion protein.
XX
SQ   Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity   85.7%;  Pred. No. 36;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              |||||||| | |||
Db          1 CATGGTCAAAAGGA 14


RESULT 31
AAX31458
ID   AAX31458 standard; DNA; 15 BP.
XX
AC   AAX31458;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Tag sequence of a transcript decreased in colorectal cancer.
XX
KW   Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
KW   diagnosis; prognosis; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   WO9853319-A2.
XX
PD   26-NOV-1998.
XX
PF   20-MAY-1998;   98WO-US010277.
XX
PR   21-MAY-1997;   97US-0047352P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1999-070161/06.
XX
PT   Use of isolated gene transcripts - useful for developing products for the
PT   diagnosis, prognosis and treatment of cancers, particularly colon and
PT   pancreatic cancer.
XX
PS   Claim 1; Page 51; 120pp; English.
XX
CC   AAX30947-31815 represent tag sequences of transcripts that are
CC   differentially expressed in colorectal cancer, in pancreatic cancer, or
CC   in both. The tag sequences can be used to identify genes by matching the
CC   tag to a gen data base member, or by using the tag sequences as probes to
CC   isolate unidentified genes from cDNA libraries. The tag sequences can
CC   also be used in a method for diagnosing colon or pancreatic cancer in a
CC   sample suspected of being neoplastic. The method comprises comparing the
CC   level of at least one transcript in a first sample of a tissue to a
CC   second sample, where the first sample is a colonic tissue suspected of
CC   being neoplastic and the second sample is a normal human colonic tissue.
CC   The transcript is identified by a tag selected from AAX30947-31815. The
CC   methods of the invention can be used in the diagnosis, prognosis and
CC   treatment of cancer
XX
SQ   Sequence 15 BP; 3 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 39;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              ||||| ||| ||||
Db          1 CATGGCCACGTGGA 14


RESULT 32
AAF51885/c
ID   AAF51885 standard; DNA; 15 BP.
XX
AC   AAF51885;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2845.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 79; 201pp; English.
```

```
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 39;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGAT 18
              ||| ||| ||||||
Db         14 ATGATCAGATGGAT 1


RESULT 33
AAF51882/c
ID   AAF51882 standard; DNA; 15 BP.
XX
AC   AAF51882;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2842.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 79; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 39;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGATGA 20
              | ||| ||||||||
Db         15 GATCAGATGGATGA 2


RESULT 34
ABK32412
ID   ABK32412 standard; DNA; 15 BP.
XX
AC   ABK32412;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human colon cancer SAGE tag #513.
XX
KW   Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW   serial analysis of gene expression; diagnostic; prognostic; probe;
KW   cancer marker; ss.
XX
OS   Homo sapiens.
XX
PN   US6333152-B1.
XX
PD   25-DEC-2001.
XX
PF   20-MAY-1998;   98US-00081646.
XX
PR   20-MAY-1998;   98US-00081646.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Zhang L,  Zhou W;
XX
DR   WPI; 2002-153821/20.
XX
PT   New human nucleic acid containing specific SAGE tags, useful as
PT   diagnostic markers for cancer, also derived probes.
XX
PS   Disclosure; Col 57; 161pp; English.
XX
CC   The invention relates to an isolated, purified human nucleic acid (I)
CC   that has the same sequence as a mRNA found in humans and is a SAGE
CC   (serial analysis of gene expression) tag comprising a single stranded
CC   probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC   diagnostic and prognostic markers of cancer, especially of the colon and
CC   pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC   SAGE tags of the invention
XX
SQ   Sequence 15 BP; 3 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 39;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          4 CATGGTCACATGGA 17
              ||||| ||| ||||
Db          1 CATGGCCACGTGGA 14
```

RESULT 35
ADQ82962/c
ID ADQ82962 standard; DNA; 14 BP.
XX
AC ADQ82962;
XX
DT 07-OCT-2004 (first entry)
XX
DE Extended hairpin tail primer #22 for SNP detection method.
XX
KW ss; primer; single nucleotide polymorphism; SNP; amplification;
KW hairpin primer; alleles; drug resistance.
XX
OS Mycobacterium tuberculosis.
XX
PN WO2004061134-A1.
XX
PD 22-JUL-2004.
XX
PF 24-DEC-2003; 2003WO-US041136.
XX
PR 27-DEC-2002; 2002US-0437165P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Alland D, Hazbon MH;
XX
DR WPI; 2004-553374/53.
XX
PT Detecting single nucleotide polymorphism (SNP) in an organism, useful for
PT identifying SNPs responsible for drug resistance, comprises amplifying a
PT nucleic acid sequence of an organism using a hairpin shaped primer.
XX
PS Example 1; SEQ ID NO 106; 53pp; English.
XX
CC The invention relates to a method of detecting a single nucleotide
CC polymorphism (SNP) in an organism by amplifying a nucleic acid sequence
CC of an organism using a hairpin shaped primer that discriminates between
CC different alleles by situating its 3' nucleotide at the location of a
CC SNP, and measuring threshold cycle or amplification efficiency or amount
CC of amplified product. A lower amplification efficiency or delayed
CC threshold cycle or a difference in the amount of amplified product is
CC indicative of a mismatch between the primer and the organism and a SNP in
CC the organism. The method is useful for efficiently identifying SNPs
CC responsible for drug resistance of infective organisms. The method and
CC kit are useful for analysing large number of isolates, thus providing a
CC means for comprehensive understanding of the frequency and position of
CC mutations in an organism. This sequence corresponds to an extended
CC hairpin tail primer used in the method of the invention
XX
SQ Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match             52.0%;  Score 10.4;  DB 1;  Length 14;
  Best Local Similarity   91.7%;  Pred. No. 43;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              |||||||||| |
Db         12 TGGTCACATGCA 1
```

RESULT 36
ADQ82964/c
ID ADQ82964 standard; DNA; 14 BP.
XX
AC ADQ82964;
XX
DT 07-OCT-2004 (first entry)
XX
DE Extended hairpin tail primer #24 for SNP detection method.
XX
KW ss; primer; single nucleotide polymorphism; SNP; amplification;
KW hairpin primer; alleles; drug resistance.
XX
OS Mycobacterium tuberculosis.
XX
PN WO2004061134-A1.
XX
PD 22-JUL-2004.
XX
PF 24-DEC-2003; 2003WO-US041136.
XX
PR 27-DEC-2002; 2002US-0437165P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Alland D, Hazbon MH;
XX
DR WPI; 2004-553374/53.
XX
PT Detecting single nucleotide polymorphism (SNP) in an organism, useful for
PT identifying SNPs responsible for drug resistance, comprises amplifying a
PT nucleic acid sequence of an organism using a hairpin shaped primer.
XX
PS Example 1; SEQ ID NO 108; 53pp; English.
XX
CC The invention relates to a method of detecting a single nucleotide
CC polymorphism (SNP) in an organism by amplifying a nucleic acid sequence
CC of an organism using a hairpin shaped primer that discriminates between
CC different alleles by situating its 3' nucleotide at the location of a
CC SNP, and measuring threshold cycle or amplification efficiency or amount
CC of amplified product. A lower amplification efficiency or delayed
CC threshold cycle or a difference in the amount of amplified product is
CC indicative of a mismatch between the primer and the organism and a SNP in
CC the organism. The method is useful for efficiently identifying SNPs
CC responsible for drug resistance of infective organisms. The method and
CC kit are useful for analysing large number of isolates, thus providing a
CC means for comprehensive understanding of the frequency and position of
CC mutations in an organism. This sequence corresponds to an extended
CC hairpin tail primer used in the method of the invention
XX
SQ Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match             52.0%;  Score 10.4;  DB 1;  Length 14;
  Best Local Similarity   91.7%;  Pred. No. 43;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              |||||||||| |
Db         12 TGGTCACATGCA 1
```

RESULT 37
AED89999/c
ID AED89999 standard; DNA; 11 BP.
XX
AC AED89999;
XX
DT 26-JAN-2006 (first entry)
XX
DE Human glucose-6-phosphate dehydrogenase wild type probe SEQ ID NO:2.
XX
KW mutation; DNA detection; glucose-6-phosphate dehydrogenase; probe; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT modified_base   1
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "5' NH2 modification"

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XX
PN   US2005266419-A1.
XX
PD   01-DEC-2005.
XX
PF   25-SEP-2004; 2004US-00949761.
XX
PR   25-SEP-2003; 2003US-0505730P.
PR   06-OCT-2003; 2003US-0509015P.
XX
PA   (MGPB-) MGP BIOTECH INC.
XX
PI   Pappas MG,  Wang Z;
XX
DR   WPI; 2005-810031/82.
XX
PT   Identifying nucleic acid mutations by obtaining a sample of target
PT   nucleic acid oligomers comprising a target sequence and detecting
PT   oligomer peaks in the fluid exiting from each of the portions of binding
PT   medium.
XX
PS   Disclosure; SEQ ID NO 2; 26pp; English.
XX
CC   The invention relates to a method for identifying nucleic acid mutations.
CC   The method comprises: (a) obtaining a sample of target nucleic acid
CC   oligomers comprising at least one target sequence; (b) loading the parts
CC   onto at least two portions of binding medium; (c) detecting oligomer
CC   peaks in the fluid exiting from each of the portions of binding medium;
CC   and (d) analyzing the oligomer peak data from the portions of binding
CC   medium. Also described is an apparatus for identifying nucleic acid
CC   mutations. The method is useful in identifying nucleic acid mutations.
CC   The present sequence represents a wild type probe for human glucose-6-
CC   phosphate dehydrogenase (G6PD), which is used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              ||||||||||
Db         11 CACATGGATG 2


RESULT 38
AAT36745/c
ID   AAT36745 standard; DNA; 14 BP.
XX
AC   AAT36745;
XX
DT   22-APR-1997  (first entry)
XX
DE   Antisense oligonucleotide to cdk4 gene.
XX
KW   Antisense; phosphorylation; retinoblastoma; tumour suppressor; ribozyme;
KW   antagonist; kinase; cyclin; cdk4; Rb; ss.
XX
OS   Synthetic.
XX
PN   DE19539130-A1.
XX
PD   29-AUG-1996.
XX
PF   20-OCT-1995;   95DE-01039130.
XX
PR   28-FEB-1995;   95DE-01008734.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Strauss M,  Bartek J,  Lukas J,  Sandig V;
XX
DR   WPI; 1996-394264/40.
XX
PT   Compsn. for treating tumour or other hyperplasias - contg. co-operative
PT   gene, antisense or ribozyme against kinase or cyclin or other inhibitor
PT   of Rb phosphorylation.
XX
PS   Claim 12; Page 4; 7pp; German.
XX
CC   The oligonucleotides AAT36744-50 represent antisense oligonucleotides
CC   targeted to genes encoding proteins that interact with, pref. by
CC   phosphorylating the retinoblastoma (Rb) protein. The oligonucleotides are
CC   used in a novel method of treating tumours by using: (a) tumour
CC   suppressor genes that co-operate with the Rb suppressor, (b) antisense or
CC   ribozymes that are antagonistic to kinases or cyclins, or (c) other
CC   compounds that inhibit Rb phosphorylation. This oligonucleotide is
CC   directed to the cyclin-dependent kinase cdk4 gene
XX
SQ   Sequence 14 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              ||||||||||
Db         14 GGTCACATGG 5


RESULT 39
AAH89017/c
ID   AAH89017 standard; DNA; 14 BP.
XX
AC   AAH89017;
XX
DT   09-SEP-2004  (revised)
DT   27-FEB-2002  (first entry)
XX
DE   Human polymorphic oligonucleotide U54701 fragment #18.
XX
KW   Human; single nucleotide polymorphic; SNP; forensic science;
KW   paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW   plant breeding; ds.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   variation       11
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200134840-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US030766.
XX
PR   10-NOV-1999;   99US-0164596P.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Au K,  Chen J,  Patil N,  Thomas D;
XX
DR   WPI; 2001-335945/35.
XX
PT   New polymorphic sites derived from the human genome are useful to
PT   determine sites correlating with phenotypic traits, particularly disease,
PT   and also in forensics and paternity testing.
XX
PS   Claim 69; Page 11; 43pp; English.
XX
CC   The present invention relates to human oligonucleotides comprising a
```

```
CC   single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC   sequence is one such oligonucleotide. The oligonucleotides can be used in
CC   forensics, paternity testing, correlation of polymorphisms with
CC   phenotypic traits, genetic mapping of phenotypic traits and marker
CC   assisted breeding of animals and crop plants
CC
CC   Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
SQ   Sequence 14 BP; 2 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match            50.0%;  Score 10;  DB 1;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 51;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGA 17
              ||||||||||
Db         10 GTCACATGGA 1


RESULT 40
ABH45285/c
ID   ABH45285 standard; DNA; 13 BP.
XX
AC   ABH45285;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 245262 for detecting SNP TSC0059887.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 245262; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match            49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  84.6%;  Pred. No. 50;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGAT 18
              |||| || ||||| .
Db         13 TGGTAACGTGGAT 1


RESULT 41
ABH45284
ID   ABH45284 standard; DNA; 13 BP.
XX
AC   ABH45284;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 245261 for detecting SNP TSC0059887.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 245261; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match            49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  84.6%;  Pred. No. 50;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGAT 18
              |||| || ||||| .
Db          1 TGGTAACGTGGAT 13


RESULT 42
ABH28185/c
ID   ABH28185 standard; DNA; 13 BP.
XX
AC   ABH28185;
XX
DT   22-FEB-2002  (first entry)
```

```
XX
DE   Oligonucleotide SEQ ID NO 228162 for detecting SNP TSC0055641.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 228162; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 50;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              || || |||||||
Db         13 GTTACGTGGATGA 1


RESULT 43
ABH28184
ID   ABH28184 standard; DNA; 13 BP.
XX
AC   ABH28184;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 228161 for detecting SNP TSC0055641.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 228161; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 50;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              || || |||||||
Db          1 GTTACGTGGATGA 13


RESULT 44
AAN70553/c
ID   AAN70553 standard; DNA; 14 BP.
XX
AC   AAN70553;
XX
DT   25-MAR-2003  (revised)
DT   29-APR-1991  (first entry)
XX
DE   Sequence of probe which corresponds to the AA sequence W-N-Y-L-D (515-
DE   519) of human tissue plasminogen activator (TPA).
XX
KW   Thrombolytic; enzyme; protease; ss.
XX
OS   Homo sapiens.
XX
PN   EP211260-A.
XX
PD   25-FEB-1987.
XX
PF   09-JUL-1986;   86EP-00109385.
XX
PR   10-JUL-1985;   85JP-00152810.
PR   31-JAN-1986;   86JP-00020469.
PR   26-APR-1986;   86JP-00097481.
XX
PA   (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.
PA   (KANF-) KANEGAFUCHI.
XX
PI   Kakutani T,  Matsumoto K,  Yahara H,  Maruyama H,  Kawaharada H;
PI   Watanabe K;
XX
DR   WPI; 1987-051507/08.
```

```
XX
PT   New chromosomal DNA coding for human tissue plasminogen activator -
PT   useful in expression vectors for high yield prodn. of activator by large
PT   scale suspension culture.
XX
PS   Example; p29; 70pp; English.
XX
CC   The probe is used in an example to exemplify the cloning of TPA gene.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 14 BP; 4 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 55;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              ||| |||| ||||
Db         14 TCACGGTCGCATG 2


RESULT 45
ADQ30064/c
ID   ADQ30064 standard; DNA; 11 BP.
XX
AC   ADQ30064;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Rat VR1 exon 1d transcription factor binding fragment #140.
XX
KW   ds; VR1 receptor; vanilloid receptor type 1; modulator;
KW   pain transmission; primary sensory neuron; transcription factor;
KW   detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;
KW   hypalgesia; hyperalgesia; neuralgia; myalgia; rat.
XX
OS   Rattus sp.
XX
PN   WO2004053120-A2.
XX
PD   24-JUN-2004.
XX
PF   01-DEC-2003; 2003WO-EP013522.
XX
PR   09-DEC-2002; 2002DE-01057421.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Weihe E,  Bieller A,  Schaefer MKH;
XX
DR   WPI; 2004-468868/44.
XX
PT   New nucleic acid that modulates expression of the vanilloid receptor-1,
PT   useful for control of pain or sensitivity disorders, comprises sequences
PT   from control regions of the receptor gene.
XX
PS   Disclosure; Page 48; 68pp; German.
XX
CC   This invention describes a novel nucleic acid containing a specific
CC   segment having at least one region that modulates expression of the VR1
CC   (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC   or fragment of this region, or a sequence that hybridises to it under
CC   standard conditions. The VR1 modulator is derived from one or more of
CC   positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC   44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC   pain, particularly in primary sensory neurons. The invention also
CC   describes a vector that contains the VR1 modulator, host cells containing
CC   this vector (other than human germ or embryonal stem cells) and a method
CC   for modulating expression of the VR1 receptor by introducing the
CC   modulator or the vector into a cell that contains the VR1 gene. The
CC   products of the invention are used for detecting a transcription factor
CC   from its binding to a regulatory sequence (or a double-stranded
CC   oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC   linked immunosorbant assay, particularly for diagnosis of diseases
CC   associated with overexpression or underexpression of the transcription
CC   factor. The region that modulates VR1 receptor expression includes a
CC   binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or
CC   GATA1. The nucleic acids of the invention, or vectors containing them,
CC   are used for prevention or treatment of pain, also for treating
CC   sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC   neuralgia and myalgia, that are associated with activity of the VR1
CC   receptor. This sequence represents a fragment of rat VR1 exon 1d DNA
CC   which is capable of binding to a transcription factor.
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 47;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||| |||||||
Db         11 TCAGGGTCACA 1


RESULT 46
AAX19072/c
ID   AAX19072 standard; DNA; 13 BP.
XX
AC   AAX19072;
XX
DT   13-MAY-1999  (first entry)
XX
DE   Human PPAR-gamma-3-E-box SEQ ID NO:41.
XX
KW   Human; peroxisome proliferator activated receptor gamma; PPAR-gamma;
KW   regulatory sequence; promoter; obesity; anorexia; lipoma; cachexia;
KW   lipodystrophy; liposarcoma; human immunodeficiency virus; HIV;
KW   insulin resistance; non-insulin-dependent diabetes mellitus;
KW   polycystic ovary syndrome; gastrointestinal tract; Crohn's disease;
KW   inflammatory bowel disease; ulcerative colitis; bowel cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9905161-A1.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998;   98WO-US015411.
XX
PR   25-JUL-1997;   97US-0053692P.
XX
PA   (LIGA-) LIGAND PHARM INC.
PA   (INSP ) INST PASTEUR.
XX
PI   Briggs MR,  Saladin RS,  Auwerx J,  Fajas L;
XX
DR   WPI; 1999-142844/12.
XX
PT   Newly isolated nucleic acid comprising a control region of a human
PT   peroxisome proliferator activated receptor (PPAR) gamma gene - useful for
PT   identifying modulators that are useful in treating diseases associated
PT   with abnormal levels of human PPAR-gamma gene expression.
XX
PS   Disclosure; Page 91; 102pp; English.
XX
CC   The present invention describes an isolated, purified or enriched nucleic
CC   acid comprising a control region of a human peroxisome proliferator
CC   activated receptor gamma (PPAR-gamma) gene. The nucleic acids are useful
CC   for screening for agents capable of modulating the expression of a human
CC   PPAR-gamma gene. These agents (modulators) form pharmaceutical
CC   compositions that are useful for treating diseases associated with
CC   high/low levels of human PPAR-gamma gene expression. The diseases include
CC   obesity, anorexia, cachexia, lipodystrophy, lipomas, liposarcomas,
CC   abnormalities associated with anti-human immunodeficiency virus (HIV)
CC   treatment, insulin resistance, non-insulin-dependent diabetes mellitus
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CC   (NIDDM), polycystic ovary syndrome, diseases of the gastrointestinal (GI)
CC   tract, inflammatory bowel disease, Crohn's disease, ulcerative colitis
CC   and bowel cancer. The nucleic acids are useful for studying the role of
CC   the PPAR-gamma gene in various diseases and disorders. The structure of
CC   PPAR-gamma enables genetic studies of PPAR- gamma mutations in humans,
CC   and evaluation of its role in disorders like insulin resistance, NIDDM,
CC   and diseases associated with altered adipose tissue function, like
CC   obesity and lipodystrophic syndromes. The nucleic acids are also useful
CC   for gene therapy and the production of transgenic animals, which are
CC   useful in screening assays. The control regions of the nucleic acids
CC   enable screening for modulators of the human PPAR-gamma gene, which are
CC   useful in designing drugs for treating disorders or diseases associated
CC   with the level of PPAR-gamma gene expression. The present sequence
CC   represents the human PPAR-gamma-3-E-box
XX
SQ   Sequence 13 BP; 4 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 59;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGAT 18
              ||||||||  ||
Db         11 GTCACATGAAT 1


RESULT 47
ADZ24722
ID   ADZ24722 standard; DNA; 13 BP.
XX
AC   ADZ24722;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human SNP detection related oligonucelotide #1689.
XX
KW   ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
KW   immune disorder; cardiovascular disease; metabolic disorder;
KW   respiratory disease; musculoskeletal disease; renal disease;
KW   nephrotropic; endocrine disease; genitourinary disease.
XX
OS   Homo sapiens.
XX
PN   WO2005030952-A1.
XX
PD   07-APR-2005.
XX
PF   30-SEP-2004; 2004WO-JP014784.
XX
PR   30-SEP-2003; 2003JP-00342519.
PR   28-MAY-2004; 2004JP-00158717.
XX
PA   (RIKE ) RIKEN KK.
PA   (STAG-) STAGEN CO LTD.
PA   (SEKI/) SEKINE A.
PA   (IIDA/) IIDA A.
PA   (SAIT/) SAITO S.
XX
PI   Sekine A,  Iida A,  Saito S,  Nakamura Y,  Kamatani N;
XX
DR   WPI; 2005-305936/31.
XX
PT   Analyzing haplotype, by detecting polymorphism in drug-related genes,
PT   electing common polymorphism (CP), building haplotype block using CP,
PT   specifying CP within block, specifying tag polymorphism from CP within
PT   block.
XX
PS   Disclosure; SEQ ID NO 1689; 1290pp; Japanese.
XX
CC   The invention relates to a method of analyzing haplotype, by detecting
CC   gene polymorphism in drug-related genes such as aryl acetylamide
CC   deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
CC   sub-family A (ABC1), member 1. The method is useful for analyzing
CC   haplotype. The method is useful for estimating the sensitivity or disease
CC   of a medicine or a foreign material, for selecting medicine for
CC   preventing or treating diseases, for determining appropriate dosage of
CC   medicine for preventing or treating a disease, for analyzing a drug
CC   interaction, and for determining the related polymorphism relative to the
CC   sensitivity of the medicine, foreign material or disease. The diseases
CC   include malignant tumor, immune disorder circulatory disease, metabolic
CC   disease, kidney disease, respiratory disease and muscle associated
CC   disease. The method enables analysis of the individual differences
CC   related to the sensitivity of a medicine, using a haplotype, without
CC   using each single nucleotide polymorphism. The present sequence
CC   represents a human SNP detection related oligonucelotide.
XX
SQ   Sequence 13 BP; 2 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 59;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCA 11
              |||||||  |||
Db          2 CCTCATGCTCA 12


RESULT 48
AED86939
ID   AED86939 standard; DNA; 13 BP.
XX
AC   AED86939;
XX
DT   12-JAN-2006  (first entry)
XX
DE   Polyamide-binding target oligonucleotide I, SEQ ID NO:12.
XX
KW   Gene expression; transcription factor inhibitor; DNA footprinting; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .13
FT                   /*tag=  a
FT                   /bound_moiety= "Bases 13-1 of SEQ ID NO:13"
FT   misc_binding    7. .10
FT                   /*tag=  b
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
XX
PN   US6958240-B1.
XX
PD   25-OCT-2005.
XX
PF   12-AUG-1999;   99US-00374704.
XX
PR   26-FEB-1996;   96US-00607078.
PR   20-FEB-1997;   97WO-US003332.
PR   08-APR-1997;   97US-0043444P.
PR   16-APR-1997;   97US-0042022P.
PR   21-APR-1997;   97US-00837524.
PR   08-MAY-1997;   97US-00853522.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Baird EE,  Dervan PB;
XX
DR   WPI; 2005-807194/82.
XX
PT   Novel polyamides comprising amino acids having N-methylpyrrole, 3-hydroxy
PT   -N-methylpyrrole and/or N-methylimidazole groups and positive patches
PT   having rigid groups adjacent to positively charged groups, useful for
PT   inhibiting gene expression.
XX
```

```
PS   Example 4; SEQ ID NO 12; 43pp; English.
XX
CC   The invention relates to a polyamide molecule which specifically binds to
CC   a predetermined site in the minor groove of a double-stranded DNA
CC   molecule in a sequence-specific manner and which contains an alpha-amino
CC   acid domain (termed the "positive patch") which contacts nucleotides in
CC   the major groove and thus inhibits the activity of major groove DNA-
CC   binding proteins. The polyamide molecule comprises one or more amino
CC   acids containing a N-methylpyrrole, 3-hydroxy-N-methylpyrrole and/or N-
CC   methylimidazole group, where one or more of these amino acid(s) are not
CC   alpha-amino acids, and a positive patch consisting of a 2 amino acid
CC   rigid group adjacent to a positively charged group (such as a positively
CC   charged amino acid). The polyamides of the invention inhibit gene
CC   expression by displacing or preventing the function of DNA-binding
CC   proteins such as transcription factors. The invention also relates to a
CC   method of inhibiting gene expression by contacting a regulatory sequence
CC   of a gene with a polyamide of the invention. The polyamide of the
CC   invention is useful for inhibiting the binding and activity of DNA-
CC   binding proteins, thus inhibiting gene expression. Sequences AED86939-
CC   AED86940 represent the two strands of a double-stranded oligonucleotide
CC   which is capable of being bound by a polyamide of the invention. This
CC   oligonucleotide was used in DNase I footprinting in an example of the
CC   invention to determine the optimum positive patch peptide sequence for
CC   inhibition of protein binding.
XX
SQ   Sequence 13 BP; 5 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match            47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity  90.9%;  Pred. No. 59;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db          3 TCATGGTCATA 13


RESULT 49
AED86940/c
ID   AED86940 standard; DNA; 13 BP.
XX
AC   AED86940;
XX
DT   12-JAN-2006  (first entry)
XX
DE   Polyamide-binding target oligonucleotide I, SEQ ID NO:13.
XX
KW   Gene expression; transcription factor inhibitor; DNA footprinting; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .13
FT                   /*tag= a
FT                   /bound_moiety= "Bases 13-1 of SEQ ID NO:12"
FT   misc_binding    4. .13
FT                   /*tag= d
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain with Arg-Pro-Arg-Arg-Arg-Arg positive
FT                   patch"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
FT   misc_binding    4. .10
FT                   /*tag= c
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain with Arg-Pro-Arg positive patch"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
FT   misc_binding    4. .9
FT                   /*tag= b
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
XX
PN   US6958240-B1.
XX
PD   25-OCT-2005.
XX
PF   12-AUG-1999;   99US-00374704.
XX
PR   26-FEB-1996;   96US-00607078.
PR   20-FEB-1997;   97WO-US003332.
PR   08-APR-1997;   97US-0043444P.
PR   16-APR-1997;   97US-0042022P.
PR   21-APR-1997;   97US-00837524.
PR   08-MAY-1997;   97US-00853522.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Baird EE,  Dervan PB;
XX
DR   WPI; 2005-807194/82.
XX
PT   Novel polyamides comprising amino acids having N-methylpyrrole, 3-hydroxy
PT   -N-methylpyrrole and/or N-methylimidazole groups and positive patches
PT   having rigid groups adjacent to positively charged groups, useful for
PT   inhibiting gene expression.
XX
PS   Example 4; SEQ ID NO 13; 43pp; English.
XX
CC   The invention relates to a polyamide molecule which specifically binds to
CC   a predetermined site in the minor groove of a double-stranded DNA
CC   molecule in a sequence-specific manner and which contains an alpha-amino
CC   acid domain (termed the "positive patch") which contacts nucleotides in
CC   the major groove and thus inhibits the activity of major groove DNA-
CC   binding proteins. The polyamide molecule comprises one or more amino
CC   acids containing a N-methylpyrrole, 3-hydroxy-N-methylpyrrole and/or N-
CC   methylimidazole group, where one or more of these amino acid(s) are not
CC   alpha-amino acids, and a positive patch consisting of a 2 amino acid
CC   rigid group adjacent to a positively charged group (such as a positively
CC   charged amino acid). The polyamides of the invention inhibit gene
CC   expression by displacing or preventing the function of DNA-binding
CC   proteins such as transcription factors. The invention also relates to a
CC   method of inhibiting gene expression by contacting a regulatory sequence
CC   of a gene with a polyamide of the invention. The polyamide of the
CC   invention is useful for inhibiting the binding and activity of DNA-
CC   binding proteins, thus inhibiting gene expression. Sequences AED86939-
CC   AED86940 represent the two strands of a double-stranded oligonucleotide
CC   which is capable of being bound by a polyamide of the invention. This
CC   oligonucleotide was used in DNase I footprinting in an example of the
CC   invention to determine the optimum positive patch peptide sequence for
CC   inhibition of protein binding.
XX
SQ   Sequence 13 BP; 4 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match            47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity  90.9%;  Pred. No. 59;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db         11 TCATGGTCATA 1


RESULT 50
ADG13736
ID   ADG13736 standard; RNA; 9 BP.
XX
AC   ADG13736;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human EGFR Amberzyme target sequence #33.
XX
KW   Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
KW   HER4; hammerhead ribozyme; inozyme; zinzyme; DNAzyme; amberzyme; cancer;
```

```
KW   brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;
KW   prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW   stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW   head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW   multidrug resistant cancer.
XX
OS   Homo sapiens.
XX
PN   US2003186909-A1.
XX
PD   02-OCT-2003.
XX
PF   21-OCT-2002; 2002US-00277494.
XX
PR   27-JAN-1997;   97US-0036749P.
PR   04-DEC-1997;   97US-00985162.
PR   22-SEP-1999;   99US-00401063.
PR   03-MAY-2001; 2001US-00848754.
PR   25-JUL-2001; 2001US-00916466.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2004-032029/03.
XX
PT   New double stranded short interfering ribonucleic acid molecule for
PT   inhibiting expression of epidermal growth factor receptor gene.
XX
PS   Claim 7; SEQ ID NO 163; 113pp; English.
XX
CC   The invention relates to a double stranded short interfering RNA (siRNA)
CC   molecule that inhibits expression of epidermal growth factor receptor
CC   (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
CC   expression vector comprising a nucleic acid sequence encoding siRNA
CC   molecule(s) in a manner that allows expression of the nucleic acid
CC   molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
CC   amberzymes zinzymes and DNAzymes. The invention is used for inhibiting
CC   expression of EGFR. It can be used for treatment of cancer, prostate
CC   cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC   cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC   cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC   cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC   life in vitro , stability, and ease of introduction of oligonucleotide to
CC   target site. The present sequence is an EGFR/HER1-4 target sequence for
CC   an siRNA of the invention.
XX
SQ   Sequence 9 BP; 2 A; 2 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 5e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCA 11
              :||:||:||
Db          1 UCAUGGUCA 9


RESULT 51
ADG13703
ID   ADG13703 standard; RNA; 10 BP.
XX
AC   ADG13703;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human EGFR Amberzyme target sequence #26.
XX
KW   Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
KW   HER4; hammerhead ribozyme; inozyme; zinzyme; DNAzyme; amberzyme; cancer;
KW   brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;
KW   prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW   stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW   head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW   multidrug resistant cancer.
XX
OS   Homo sapiens.
XX
PN   US2003186909-A1.
XX
PD   02-OCT-2003.
XX
PF   21-OCT-2002; 2002US-00277494.
XX
PR   27-JAN-1997;   97US-0036749P.
PR   04-DEC-1997;   97US-00985162.
PR   22-SEP-1999;   99US-00401063.
PR   03-MAY-2001; 2001US-00848754.
PR   25-JUL-2001; 2001US-00916466.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2004-032029/03.
XX
PT   New double stranded short interfering ribonucleic acid molecule for
PT   inhibiting expression of epidermal growth factor receptor gene.
XX
PS   Claim 7; SEQ ID NO 130; 113pp; English.
XX
CC   The invention relates to a double stranded short interfering RNA (siRNA)
CC   molecule that inhibits expression of epidermal growth factor receptor
CC   (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
CC   expression vector comprising a nucleic acid sequence encoding siRNA
CC   molecule(s) in a manner that allows expression of the nucleic acid
CC   molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
CC   amberzymes zinzymes and DNAzymes. The invention is used for inhibiting
CC   expression of EGFR. It can be used for treatment of cancer, prostate
CC   cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC   cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC   cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC   cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC   life in vitro , stability, and ease of introduction of oligonucleotide to
CC   target site. The present sequence is an EGFR/HER1-4 target sequence for
CC   an siRNA of the invention.
XX
SQ   Sequence 10 BP; 3 A; 2 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 49;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCA 11
              :||:||:||
Db          1 UCAUGGUCA 9


RESULT 52
AAN80414/c
ID   AAN80414 standard; DNA; 11 BP.
XX
AC   AAN80414;
XX
DT   25-MAR-2003  (revised)
DT   16-OCT-1990  (first entry)
XX
DE   Linker.
XX
KW   Human interferon-1; ds.
XX
OS   Synthetic.
XX
PN   DD250335-A.
XX
PD   08-OCT-1987.
```

XX
PF 31-JAN-1986; 86DD-00286634.
XX
PR 31-JAN-1986; 86DD-00286634.
XX
PA (DEAK) AKAD WISSENSCHAFTEN DDR.
XX
PI Hartmann M, Reichardt W, Walter F, Birchhirsc ETM;
XX
DR WPI; 1988-056899/09.
XX
PT Prodn. of expression plasmid for mature human interferon alpha - from
PT series of intermediate plasmids contg. separate C and N terminal gene
PT regions derived from single gene bank clone.
XX
PS Claim 1; Page 1; 18pp; German.
XX
CC This linker is part of a pair which is attached to the N-terminal of a
CC fragment contg. the human interferon alpha-1 gene. A 207 bp prod. with a
CC BamHI terminal is the result. This provides fer matching to expression
CC regulatory signals and, since 2 promoters can be incorporated into the
CC final vector, a high level of expression is obtained. The 5' end of this
CC strand overhangs the 3' end of the complementary strand by GATC. The 5'
CC end of the complementary strand overhangs the 3' end of the sense strand
CC by CTAG. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR
CC -2003 to correct PI field.)
XX
SQ Sequence 11 BP; 2 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CACATGGAT 18
|||||||||
Db 10 CACATGGAT 2

RESULT 53
AAZ18812/c
ID AAZ18812 standard; DNA; 11 BP.
XX
AC AAZ18812;
XX
DT 22-OCT-1999 (first entry)
XX
DE Murine C57BL/6 SAGE tag 2340946.
XX
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
OS Mus sp.
XX
PN WO9941364-A2.
XX
PD 19-AUG-1999.
XX
PF 12-FEB-1999; 99WO-US002962.
XX
PR 13-FEB-1998; 98US-0074737P.
PR 26-AUG-1998; 98US-0097937P.
PR 28-SEP-1998; 98US-0102051P.
XX
PA (WIST-) WISTAR INST.
XX
PI Heber-Katz E;
XX
DR WPI; 1999-494533/41.
XX
PT New mammalian model for enhanced wound healing - useful for identifying
PT enhanced wound healing genes.
XX
PS Claim 13; Page 57; 136pp; English.
XX
CC This invention describes a novel non-MRL healer mouse (M) having at least
CC one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by
CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention
XX
SQ Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGGTCACAT 14
|||||||||
Db 10 TGGTCACAT 2

RESULT 54
ABK99449
ID ABK99449 standard; DNA; 11 BP.
XX
AC ABK99449;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human CYP3A5 gene polymorphic variant DNA sequence #37.
XX
KW Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW AIDS; African American; forensic marker; pharmacological; cytostatic;
KW antidiabetic; anti-HIV; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200253775-A2.
XX
PD 11-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-EP015290.
XX
PR 28-DEC-2000; 2000EP-00128627.
PR 28-DEC-2000; 2000US-0258684P.
PR 29-DEC-2000; 2000US-0258952P.
PR 16-JAN-2001; 2001EP-00100172.
PR 18-JAN-2001; 2001US-0262859P.
PR 16-AUG-2001; 2001EP-00118884.
PR 16-AUG-2001; 2001US-0312825P.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Haberl M, Hustert E;
XX
DR WPI; 2002-583628/62.
XX
PT Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT cardiovascular diseases, diabetes and AIDS, and for identifying
PT polymorphisms.
XX
PS Claim 1; Page 50; 138pp; English.

```
XX
CC   The present invention relates to a new CYP3A5 polynucleotide encoding a
CC   polypeptide, where the polynucleotide is capable of hybridising to a
CC   CYP3A5 gene. The invention is useful in an in vitro method for
CC   identifying a polymorphism. The invention is also useful for useful for
CC   diagnosing a disorder related to the presence of a molecular variant of a
CC   CYP3A5 or susceptibility to such a disorder, where the disorder is
CC   cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC   The invention can further be used for the preparation of a diagnostic
CC   composition for diagnosing a disease in a subject having a genome
CC   comprising a variant allele of the CYP3A5 gene, where the subject is an
CC   African American. The molecules of the invention are as forensic markers
CC   and in pharmacological studies. The present nucleic acid sequence
CC   represents a human CYP3A5 gene polymorphism variant DNA sequence, as
CC   described in the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCACATGGA 17
              |||||||||
Db          2 TCACATGGA 10


RESULT 55
AAQ88597/c
ID   AAQ88597 standard; DNA; 12 BP.
XX
AC   AAQ88597;
XX
DT   21-DEC-1995  (first entry)
XX
DE   Human mitochondrial D-loop region DNA probe 6-10.
XX
KW   Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
KW   D-loop region; biological chip; hybridisation fingerprint;
KW   interrogation position; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    12
FT                    /*tag=  a
FT                    /note= "3'-end of probe is covalently attached to chip
FT                    surface"
XX
PN   WO9511995-A1.
XX
PD   04-MAY-1995.
XX
PF   26-OCT-1994;    94WO-US012305.
XX
PR   26-OCT-1993;    93US-00143312.
PR   02-AUG-1994;    94US-00284064.
XX
PA   (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI   Chee M,  Cronin MT,  Fodor SP,  Gingeras TR,  Huang XC,  Hubbell EA;
PI   Lipshutz RJ,  Lobban PE,  Miyada CG,  Morris MS,  Shah N,  Sheldon EL;
XX
DR   WPI; 1995-178887/23.
XX
PT   New arrays of oligo:nucleotide probes - used for comparing known
PT   sequences with variants for detection of mutation(s) and sequencing.
XX
PS   Disclosure; Page 108; 223pp; English.
XX
CC   A DNA chip was prepared for analysing sequences contained in a 1.3kb
CC   fragment of human mitochondrial DNA from the D-loop region, the most
CC   polymorphic region of human mitochondrial DNA. The chip comprised a set
CC   of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
CC   varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
CC   x 1cm array. Each position in the sequence was represented by at least
CC   one probe (usually 2 or more). DNA was amplified from six human donors
CC   and then transcribed to give the 1.3kb RNA transcripts which were
CC   fragmented and hybridised to the chip. For each individual, a unique
CC   hybridisation fingerprint was produced on the chip; all differences could
CC   be correlated with differences in the cloned genomic DNA sequence
XX
SQ   Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               |||||||||
Db          11 CATGGATGA 3


RESULT 56
AAV32269
ID   AAV32269 standard; DNA; 12 BP.
XX
AC   AAV32269;
XX
DT   18-AUG-1998  (first entry)
XX
DE   Random primed reverse transcription PCR primer 114.
XX
KW   RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
KW   differential gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO9813521-A1.
XX
PD   02-APR-1998.
XX
PF   26-SEP-1997;   97WO-EP005290.
XX
PR   27-SEP-1996;   96GB-00020216.
XX
PA   (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX
PI   Consalez G,  Fesce R;
XX
DR   WPI; 1998-230725/20.
XX
PT   Differential screening of gene expression by reverse transcription
PT   polymerase chain reaction - uses random priming with primers selected for
PT   high efficiency and selectivity by computer screening of database(s).
XX
PS   Claim 9; Page 24; 37pp; English.
XX
CC   The invention provides a method for the differential screening of gene
CC   expression by random primed reverse transcription PCR (RT-PCR). The
CC   primer sequences are generated by stimulating PCR reactions on non-
CC   redundant mammalian nucleotide sequence databank entries containing at
CC   least 1,000 bp of coding region. The primers selected, such as the
CC   present one, had to meet various criteria such as having an efficiency
CC   index between 2-10, having a selectivity index higher than 1, being 12 bp
CC   long i.e. 8 C or G and 4 T or A, and each primer differed from the others
CC   in at least 5 of the 8 bases at the 3'-end. The invention claims the
CC   selected primers make it possible to use internally primed, PCR-based RNA
CC   fingerprinting for simple, exhaustive and systematic analysis of
CC   differential gene expression as an advantageous alternative to
CC   differential display. The method can also be useful for isolating new
CC   coding sequences and to compare known and new genes
XX
SQ   Sequence 12 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 1 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
```

```
  Best Local Similarity   81.8%;  Pred. No. 63;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGG 16
              ||||||| ||:
Db          2 TGGTCACGTGS 12


RESULT 57
AAH23540/c
ID   AAH23540 standard; DNA; 12 BP.
XX
AC   AAH23540;
XX
DT   03-AUG-2001  (first entry)
XX
DE   Antibacterial peptide nucleic acid oligonucleotide #49.
XX
KW   Peptide nucleic acid; PNA; antimicrobial; antibiotic; cationic peptide;
KW   antisense; disinfectant; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "linked to AAB99988 by 8-amino-3,6-dioxaoctanoic
FT                   acid"
XX
PN   WO200127262-A1.
XX
PD   19-APR-2001.
XX
PF   13-OCT-2000; 2000WO-DK000581.
XX
PR   13-OCT-1999;   99DK-00001468.
PR   15-OCT-1999;   99US-0159683P.
XX
PA   (PANT-) PANTHECO AS.
XX
PI   Nielsen PE,  Schou C,  Wissenbach M;
XX
DR   WPI; 2001-290722/30.
XX
PT   Identifying target genes in a microorganism (e.g. Escherichia coli) as a
PT   basis for anti-infective treatment comprises selecting potential targets
PT   known to be present and obtaining complementary (antisense) peptide
PT   nucleic acid sequences.
XX
PS   Example 3; Page 35; 57pp; English.
XX
CC   The present invention describes a method of identifying target genes, for
CC   use in anti-infective treatments, in a microorganism, involving obtaining
CC   antisense peptide nucleic acid (PNA) sequences for potential target
CC   genes, mixing them with the organism in culture and comparing the growth
CC   in the presence and absence of the antisense PNA sequence, where a useful
CC   target gene is one which results in decreased growth when blocked by the
CC   antisense sequence. Antisense oligonucleotides are linked to cationic
CC   peptides via a linking group for use as antimicrobial compounds,
CC   particularly as antibiotics. The present sequence is an oligonucleotide
CC   useful as the antisense portion of a PNA in the present invention
XX
SQ   Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 69;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGAT 18
              |||||| ||| |
Db         12 GGTCACGTGGTT 1


RESULT 58
ABH82120
ID   ABH82120 standard; DNA; 12 BP.
XX
AC   ABH82120;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 282113 for detecting SNP TSC0010416.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 282113; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 69;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              |||| | |||||
Db          1 TGGTTATATGGA 12


RESULT 59
ABI08296
ID   ABI08296 standard; DNA; 12 BP.
XX
AC   ABI08296;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 308269 for detecting SNP TSC0022931.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

```
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 308269; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 69;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCAC 12
              ||||||  ||||
Db          1 CCTCATCCTCAC 12


RESULT 60
ADW11578
ID   ADW11578 standard; RNA; 12 BP.
XX
AC   ADW11578;
XX
DT   24-MAR-2005  (first entry)
XX
DE   siRNA production-related p4 box RNA SeqID15.
XX
KW   short interfering RNA; siRNA; RNA interference; ribozyme; ss.
XX
OS   Unidentified.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .4
FT                   /*tag=  b
FT                   /bound_moiety= "Itself"
FT                   /note= "Binds nucleotides 12-9 of itself"
FT   misc_binding    9. .12
FT                   /*tag=  b
FT                   /bound_moiety= "Itself"
FT                   /note= "Binds nucleotides 4-1 of itself"
XX
PN   WO2005001039-A2.
XX
PD   06-JAN-2005.
XX
PF   28-MAY-2004; 2004WO-US017034.
XX
PR   29-MAY-2003; 2003US-0474001P.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
PI   Soukup GA,  Kertsburg A;
XX
DR   WPI; 2005-075534/08.
XX
PT   Producing a small, interfering RNA (siRNA) by providing a first or second
PT   RNA construct comprising a first or second ribozyme operably linked to a
PT   sense or an antisense strand, respectively of an siRNA.
XX
PS   Example 1; SEQ ID NO 15; 43pp; English.
XX
CC   This invention relates to a novel method of producing a small interfering
CC   RNA (siRNA). The method comprises providing a first RNA construct
CC   comprising a first ribozyme operably linked to a sense and antisense
CC   strand of an siRNA and placing the first and second RNA constructs under
CC   conditions where the first and second ribozyme catalyze the cleavage of
CC   the sense and antisense strands of the siRNA from the first and second
CC   RNA constructs. The present sequence is that of a p4 box RNA which was
CC   used during the exemplification of the method of the invention.
XX
SQ   Sequence 12 BP; 5 A; 2 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 69;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATG 15
              ||:||  |||:|
Db          1 CAUGGAAACAUG 12


RESULT 61
AAX32635
ID   AAX32635 standard; DNA; 10 BP.
XX
AC   AAX32635;
XX
DT   23-JUN-1999  (first entry)
XX
DE   Anticancer duplex forming oligonucleotide SEQ ID #35.
XX
KW   Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW   multiple drug resistance; MDR; ss.
XX
OS   Synthetic.
XX
PN   WO9523162-A1.
XX
PD   31-AUG-1995.
XX
PF   27-FEB-1995;   95WO-US002419.
XX
PR   28-FEB-1994;   94US-00202927.
XX
PA   (MICR-) MICROPROBE CORP.
PA   (UYYA ) UNIV YALE.
XX
PI   Cheng Y,  Lukhtanov EA,  Meyer RB,  Pai BS,  Reed MW,  Zhou JH;
XX
DR   WPI; 1995-311501/40.
XX
PT   New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT   intramolecular duplex with hairpin loop region, having selective
PT   cytotoxicity against some tumour cells.
```

```
XX
PS   Disclosure; Page 57; 107pp; English.
XX
CC   New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC   and which have a steroid structure attached to the 3'-end through a
CC   linker attached to the A-ring of the steroid skeleton. In particular, the
CC   present sequence has a cholesterol moiety attached by its A-ring to to
CC   the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC   of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC   oligonucleotides form stable duplexes at physiological temperature and
CC   have selective cytotoxic activity against certain tumour cell lines,
CC   including some with multiple drug resistance
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              |||| |||||
Db          1 CACACGGATG 10


RESULT 62
AAX32631
ID   AAX32631 standard; DNA; 10 BP.
XX
AC   AAX32631;
XX
DT   23-JUN-1999  (first entry)
XX
DE   Anticancer duplex forming oligonucleotide SEQ ID #31.
XX
KW   Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW   multiple drug resistance; MDR; ss.
XX
OS   Synthetic.
XX
PN   WO9523162-A1.
XX
PD   31-AUG-1995.
XX
PF   27-FEB-1995;   95WO-US002419.
XX
PR   28-FEB-1994;   94US-00202927.
XX
PA   (MICR-) MICROPROBE CORP.
PA   (UYYA ) UNIV YALE.
XX
PI   Cheng Y,  Lukhtanov EA,  Meyer RB,  Pai BS,  Reed MW,  Zhou JH;
XX
DR   WPI; 1995-311501/40.
XX
PT   New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT   intramolecular duplex with hairpin loop region, having selective
PT   cytotoxicity against some tumour cells.
XX
PS   Disclosure; Page 56; 107pp; English.
XX
CC   New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC   and which have a steroid structure attached to the 3'-end through a
CC   linker attached to the A-ring of the steroid skeleton. In particular, the
CC   present sequence has a cholesterol moiety attached by its A-ring to to
CC   the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC   of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC   oligonucleotides form stable duplexes at physiological temperature and
CC   have selective cytotoxic activity against certain tumour cell lines,
CC   including some with multiple drug resistance
XX
SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              |||||| ||
Db          1 CACATGGGTG 10


RESULT 63
AAQ96927/c
ID   AAQ96927 standard; DNA; 10 BP.
XX
AC   AAQ96927;
XX
DT   16-OCT-2003  (revised)
DT   26-MAR-1996  (first entry)
XX
DE   HIV-1 NL4-3 nef gene nucleotide deletion 522.
XX
KW   HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9521912-A1.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-AU000063.
XX
PR   14-FEB-1994;   94AU-00003864.
PR   21-FEB-1994;   94AU-00004002.
PR   23-DEC-1994;   94AU-00000284.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA   (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI   Deacon NJ,  Learmont JC,  Mcphee DA,  Crowe S,  Cooper D;
XX
DR   WPI; 1995-293115/38.
XX
PT   New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT   LTR region - can be used in a vaccine to inhibit/reduce productive
PT   infection in an individual by a pathogenic strain.
XX
PS   Claim 13; Page 195; 301pp; English.
XX
CC   Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC   more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC   decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC   AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC   resulting avirulent HIV strains are still capable of inducing an immune
CC   response in humans, and enable the generation of therapeutic, diagnostic
CC   and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         10 CTCAGGGTCA 1


RESULT 64
AAH63224
ID   AAH63224 standard; cDNA; 10 BP.
XX
AC   AAH63224;
XX
DT   20-SEP-2001  (first entry)
```

XX
DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 64.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 1; Page 40; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 3 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          9 TCACATGGAT 18
              |||||| |||
Db          1 TCACATTGAT 10
```

RESULT 65
AAF38625
ID AAF38625 standard; DNA; 10 BP.
XX
AC AAF38625;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5364.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 191; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         11 ACATGGATGA 20
               | ||||||||
Db          1 AAATGGATGA 10
```

RESULT 66
AAF41055/c
ID AAF41055 standard; DNA; 10 BP.
XX
AC AAF41055;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7794.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.

XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 278; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TGGTCACATG 15
||||||||.|
Db 10 TGGTCACAGG 1

RESULT 67
AAS98404
ID AAS98404 standard; DNA; 10 BP.
XX
AC AAS98404;
XX
DT 12-MAR-2002 (first entry)
XX
DE Galanin receptor gene GALR1 allele-specific oligonucleotide #116.
XX
KW Galanin receptor; GALR1; human; single nucleotide polymorphism; SNP;
KW drug discovery; haplotyping; infectious diarrhoea;
KW growth hormone deficiency; allele-specific oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200179237-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US012306.
XX
PR 14-APR-2000; 2000US-0197838P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
XX
DR WPI; 2002-066341/09.
XX
PT Genotyping human galanin receptor gene of an individual for determining
PT haplotype of an individual, involves determining the identity of
PT nucleotide pair at specific polymorphic sites for two copies of the gene.
XX
PS Claim 18; Page 16; 99pp; English.
XX
CC The invention relates to genotyping human galanin receptor (GALR1) gene
CC of an individual, involving determining for the two copies of the GALR1
CC gene present in the individual, the identity of the nucleotide pair at
CC one or more polymorphic sites. The method is useful for determining
CC whether an individual has a haplotype or haplotype pairs defined in the
CC specification. This is useful for improving the efficacy and reliability
CC of several steps in the discovery and development of drugs for treating
CC diseases associated with GALR1 activity, e.g., infectious diarrhoea and
CC growth hormone deficiency, to validate GALR1 as a candidate agent for
CC treating a specific condition or disease predicted to be associated with
CC GALR1 activity, and in the design of clinical trials of candidate drugs
CC for treating a specific condition or disease predicted to be associated
CC with GALR1 activity. The method is useful to screen for compounds
CC targeting GALR1 to treat a specific conditions or disease associated with
CC GALR1 activity. A GALR1 polynucleotide or variant is useful in studying
CC the expression and function of GALR1, and in expressing GALR1 protein for
CC use in screening for candidate drugs to treat diseases related to GALR1
CC activity. The polynucleotide or variant is useful for studying expression
CC of the GALR1 isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against GALR1 protein, and for studying the effect of the
CC variation on the biological activity of GALR1 as well as on the binding
CC affinity of candidate drugs targeting GALR1 for the treatment of
CC infectious diarrhoea and growth hormone insufficiency. AAS98289- AAS98408
CC represent human GALR1 gene allele-specific oligonucleotides used to
CC detect GALR1 gene polymorphisms as described in the method of the
CC invention
XX
SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACATGGATGA 20
.|||||||
Db 1 AGATGGATGA 10

RESULT 68
AAD26025
ID AAD26025 standard; DNA; 10 BP.
XX
AC AAD26025;
XX
DT 26-MAR-2002 (first entry)
XX
DE Primer #27 to detect human PI4 gene polymorphisms.
XX
KW Human; protease inhibitor; PI4; kallistatin; therapy; polymorphic site;
KW PS; haplotyping; genotyping; acute pancreatitis; drug screening;
KW antiinflammatory; chromosome 14q31-q32.1; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200179227-A2.
XX

PD 25-OCT-2001.
XX
PF 13-APR-2001; 2001WO-US012255.
XX
PR 13-APR-2000; 2000US-0196990P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Koshy B, Sanchis A;
XX
DR WPI; 2002-075060/10.
XX
PT Genotyping protease inhibitor 4 gene of individual for determining
PT haplotype of individual, involves determining identity of nucleotide pair
PT at specific polymorphic sites for two copies of gene.
XX
PS Claim 18; Page 14; 79pp; English.
XX
CC The present invention relates to genotyping protease inhibitor (PI) 4
CC (kallistatin) gene of an individual, involves determining for the two
CC copies of the PI4 gene present in the individual, the identity of the
CC nucleotide pair at one or more polymorphic sites. PI4 gene is located on
CC chromosome 14q31-q32.1. Genotyping is useful for determining if an
CC individual has a haplotype or haplotype pairs defined in the
CC specification. Haplotyping is useful for improving the efficacy and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with PI4 activity, e.g. acute
CC pancreatitis, to validate PI4 as a candidate agent for treating a
CC specific condition or disease predicted to be associated with PI4
CC activity, and in the design of clinical trials of candidate drugs for
CC treating a specific condition or disease predicted to be associated with
CC PI4 activity. The PI4 gene is useful in studying the expression and
CC function of PI4, and in expressing PI4 protein for use in screening for
CC candidate drugs to treat diseases related to PI4 activity. The present
CC sequence is a primer to detect human PI4 gene polymorphisms
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACATGGATGA 20
|| |||||||
Db 1 ACGTGGATGA 10

RESULT 69
ABK55547/c
ID ABK55547 standard; DNA; 10 BP.
XX
AC ABK55547;
XX
DT 18-JUN-2002 (first entry)
XX
DE Selectin L Lymphocyte Adhesion Molecule 1 (SELL) oligonucleotide #83.
XX
KW Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL;
KW neonatal pertussis; whooping cough; haplotyping; primer;
KW allele-specific oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200216654-A1.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026675.
XX
PR 25-AUG-2000; 2000US-0228262P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Bieglecki KM, Kliem SE, Koshy B, Kumar AM;
XX
DR WPI; 2002-292071/33.
XX
PT Novel genetic variants of selectin L lymphocyte adhesion molecule 1
PT (SELL) gene useful for therapeutic purposes and for expressing SELL
PT protein useful in identifying drugs to treat whooping cough.
XX
PS Claim 19; Page 15; 137pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence which is a polymorphic variant of a reference
CC sequence for Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene. SELL
CC polypeptide is useful for screening for drugs targeting the polypeptide.
CC Oligonucleotides derived from (I) are used to target SELL and a haplotype
CC or haplotype pair of SELL gene. These are useful in developing diagnostic
CC tests and therapeutic treatments for neonatal pertussis (whooping cough).
CC (I) is useful for studying the expression and function of SELL and
CC expressing SELL protein for use in screening for candidate drugs to treat
CC diseases related to SELL activity. The polymorphism and haplotype data
CC are useful for validating whether SELL is a suitable target for drugs to
CC treat whooping cough, screening for such drugs and reducing bias in
CC clinical trials of such drugs. Establishing the SELL haplotype or
CC haplotype pair of an individual is useful for improving the efficiency
CC and reliability of several steps in the discovery and development of
CC drugs for treating diseases associated with SELL activity e.g. neonatal
CC pertussis (whooping cough). The haplotyping method is useful to validate
CC SELL as a candidate target for treating a specific condition or disease
CC predicted to be associated with SELL activity. The method is also useful
CC in screening for compounds targeting SELL to treat a specific condition
CC or disease predicted to be associated with SELL activity, e.g. detecting
CC which of the SELL haplotypes or haplotype pairs present in individual
CC members of a population with the specific disease of interest enables one
CC to screen for compounds that display the highest desired agonist or
CC antagonist activity for each of the most frequent SELL isoforms present
CC in the disease population. A polymorphic variant of SELL is useful in
CC studying the effect of the variation on the biological activity of SELL,
CC on the binding affinity of candidate drugs targeting SELL for the
CC treatment of neonatal pertussis (whooping cough) and in assays to measure
CC the binding affinities of one or more candidate drugs targeting the SELL
CC protein. ABK55465-ABK55559 represent SELL gene allele-specific
CC oligonucleotides of the invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TGGTCACATG 15
||||| ||||
Db 10 TGGTCTCATG 1

RESULT 70
AAD31708
ID AAD31708 standard; RNA; 10 BP.
XX
AC AAD31708;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human CD39L2 initiation start site #2.
XX
KW Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency;
KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;

```
KW   dermatological; immunosuppressive; vulnerary; nootropic; anticonvulsant;
KW   antiinflammatory; nephrotropic; gastrointestinal; vasotropic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_signal     7. .9
FT                   /*tag= a
FT                   /note= "Initiation codon"
XX
PN   US6350447-B1.
XX
PD   26-FEB-2002.
XX
PF   29-JAN-1999;   99US-00240639.
XX
PR   29-JAN-1999;   99US-00240639.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Chadwick BP,  Frischauf A;
XX
DR   WPI; 2002-215262/27.
XX
PT   An isolated polypeptide with phosphohydrolase activity, designated
PT   CD39L2, useful to identify other proteins with which binding occurs or
PT   identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
PT   sclerosis and osteoporosis.
XX
PS   Example; Col 56; 101pp; English.
XX
CC   The present invention relates to novel proteins with phosphohydrolase
CC   activity, designated CD-39-like (CD39L) proteins and polynucleotides
CC   encoding such proteins. CD39L proteins are useful to treat infectious
CC   diseases caused by viral, bacterial, fungal or other infection that may
CC   be treatable with CD39L. They are useful in the treatment of various
CC   immune deficiencies and disorders, autoimmune disorders such as multiple
CC   sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
CC   thyroiditis and insulin dependent diabetes mellitus, allergic reactions
CC   and conditions such as asthma and other respiratory problems, periodontal
CC   disease, osteoporosis, osteoarthritis and other tooth repair processes.
CC   They may have utility in compositions used for bone, cartilage, tendon,
CC   ligament and/or nerve tissue growth or regeneration as well as for wound
CC   healing and tissue repair and replacement and in the treatment of burns,
CC   incisions and ulcers. CD39L proteins may also be useful for proliferation
CC   of neural cells and for regeneration of nerve and brain tissue, i.e. for
CC   the treatment of central nervous system diseases such as Alzheimer's
CC   disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
CC   disease, peripheral nervous system diseases peripheral nerve injuries,
CC   peripheral neuropathy and localised neuropathies. They are also used to
CC   treat mechanical and traumatic disorders which involve degeneration,
CC   death or trauma to neural cells or nerve tissue. CD39L proteins of the
CC   invention are also useful to promote better or faster closure of non-
CC   healing wounds, including pressure ulcers, ulcers associated with
CC   vascular insufficiency and surgical and traumatic wounds. They also
CC   exhibit anti-inflammatory activity and may be used to treat inflammatory
CC   conditions including chronic or acute conditions), including ischaemia-
CC   reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
CC   or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
CC   disease. The present sequence is human CD39L2 initiation start site
XX
SQ   Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 64;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10
```

RESULT 71

```
AAS95414
ID   AAS95414 standard; DNA; 10 BP.
XX
AC   AAS95414;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human ICAM2 gene allele-specific oligonucleotide PCR primer #19.
XX
KW   Human; intercellular adhesion molecule 2; ICAM2; haplotyping; ss;
KW   haplotype pair; single nucleotide polymorphism; genotyping; PCR primer;
KW   gene therapy; drug screening; anti-HIV; antiinflammatory; probe;
KW   human immunodeficiency virus; sequencing primer.
XX
OS   Homo sapiens.
XX
PN   WO200185918-A1.
XX
PD   15-NOV-2001.
XX
PF   07-MAY-2001; 2001WO-US014714.
XX
PR   05-MAY-2000; 2000US-0201946P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Denton RR,  Kliem SE,  Lee HH,  Nandabalan K;
XX
DR   WPI; 2002-055590/07.
XX
PT   Novel polynucleotide containing polymorphisms in intercellular adhesion
PT   molecule 2 gene, useful in developing drugs for treating human
PT   immunodeficiency virus infection and inflammatory diseases.
XX
PS   Claim 18; Page 14; 81pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding human intercellular adhesion molecule 2 (ICAM2). A method for
CC   haplotyping the ICAM2 gene in an individual comprises identifying the
CC   nucleotide at one or more polymorphic sites and determining whether one
CC   of the copies of the gene is defined by one of the ICAM2 haplotypes given
CC   in the specification or whether both copies are defined by a haplotype
CC   pair. This method is useful in genotyping, whereby all possible haplotype
CC   pairs can be assigned to specific genotypes. An association between a
CC   trait and a haplotype or haplotype pair of the ICAM2 gene can be
CC   identified by comparing the frequency of the haplotype or haplotype pair
CC   in a population exhibiting the trait with the frequency of the haplotype
CC   or haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. ICAM2 and its corresponding DNA are used
CC   for studying the expression and function of ICAM2, for use in screening
CC   for candidate drugs to treat diseases related to ICAM2 activity, such as
CC   HIV infection and inflammatory diseases. The sequences are also useful
CC   for studying the effect of variation on the biological activity of ICAM2
CC   as well as on the binding affinity of candidate drugs targeting ICAM2.
CC   Sequences AAS95362-AAS95417 and AAS95419-AAS95442 represent allele-
CC   specific oligonucleotide probes, sequencing primers, PCR primers and cDNA
CC   encoding human ICAM2
XX
SQ   Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||| |||||
Db          1 TCATAGTCAC 10
```

RESULT 72

```
ABV84769/c
ID   ABV84769 standard; cDNA; 10 BP.
```

```
XX
AC   ABV84769;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Chronic hepatitis C/HCC differentially expressed gene SAGE tag #579.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 46; Page 26; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84691-ABV84790 are SAGE tags representing the 100 least highly
CC   expressed genes out of those genes which are underexpressed in
CC   hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX
SQ   Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db         10 CTCTTGGTCA 1


RESULT 73
ABV84230/c
ID   ABV84230 standard; cDNA; 10 BP.
XX
AC   ABV84230;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human chronic hepatitis C tissue overexpressed gene SAGE tag #40.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 1; Page 10; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84191-ABV84290 are SAGE tags representing the 100 most highly
CC   expressed genes out of those genes which are overexpressed in chronic
CC   hepatitis C liver tissue compared with normal liver tissue
XX
SQ   Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db         10 CTCTTGGTCA 1


RESULT 74
ABK09446
ID   ABK09446 standard; DNA; 10 BP.
XX
AC   ABK09446;
XX
DT   14-MAR-2002  (first entry)
XX
DE   Human NPR1 gene allele-specific oligonucleotide PCR primer #26.
XX
KW   Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; ss;
KW   atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
KW   haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
KW   drug screening; hypertension; hypotensive; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200179231-A2.
XX
```

PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US012300.
XX
PR 14-APR-2000; 2000US-0197330P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Choi JY, Kliem SE, Nandabalan K;
XX
DR WPI; 2002-066340/09.
XX
PT Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of
PT an individual, involves determining identity of nucleotide pair at
PT specific polymorphic sites for two copies of the gene.
XX
PS Claim 17; Page 15; 96pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human natriuretic peptide receptor A/guanylate cyclase A
CC (atrionatriuretic peptide receptor A) or NPR1 polypeptide. A method for
CC haplotyping the NPR1 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the NPR1 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the NPR1 gene can be
CC identified by comparing the frequency of the haplotype or haplotype pair
CC in a population exhibiting the trait with the frequency of the haplotype
CC or haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. NPR1 and its corresponding DNA are used
CC for studying the expression and function of NPR1, for use in screening
CC for candidate drugs to treat diseases related to NPR1 activity, such as
CC hypertension. The sequences are also useful for studying the effect of
CC variation on the biological activity of NPR1 as well as on the binding
CC affinity of candidate drugs targeting NPR1. Sequences AAS99959-AAS99990
CC and ABK09390-ABK09462 represent probes, sequencing primers and PCR
CC primers used to detect NPR1 gene polymorphisms
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CATGGTCACA 13
|| |||||||
Db 1 CAAGGTCACA 10

RESULT 75
AAS16822
ID AAS16822 standard; DNA; 10 BP.
XX
AC AAS16822;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human apolipoprotein C1 (APOC1) gene PCR primer #8.
XX
KW Human; apolipoprotein C1; APOC1; single nucleotide polymorphism;
KW haplotyping; haplotype pair; hypercholesterolaemia; nootropic; SDAT; ss;
KW senile dementia of Alzheimer's type; neuroprotective; antilipaemic;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200177129-A2.
XX
PD 18-OCT-2001.
XX
PF 10-APR-2001; 2001WO-US011808.
XX
PR 11-APR-2000; 2000US-0196545P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
XX
DR WPI; 2002-041286/05.
XX
PT New haplotypes of the human apolipoprotein C1 gene, useful to detect and
PT find treatment for disease associated with its activity such as
PT hypercholestrolemia and Alzheimer's disease.
XX
PS Claim 18; Page 13; 51pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the human
CC apolipoprotein C1 (APOC1) gene. Haplotyping the APOC1 gene of an
CC individual, comprises determining if the individual has one of the APOC1
CC haplotypes or haplotype pairs fully defined in the specification.
CC Genotyping the APOC1 gene of an individual, comprises determining the
CC identity of the nucleotide pair at one or more polymorphic sites and
CC predicting a haplotype pair for the APOC1 gene of an individual by
CC enumerating all possible haplotype pairs which are consistent with the
CC genotype, comparing the possible haplotype pairs to the data detailed in
CC the specification and assigning a haplotype pair to the individual that
CC is consistent with the data. Identifying an association between a trait
CC and a haplotype or haplotype pair of the APOC1 gene, comprises comparing
CC the frequency of the haplotype/haplotype pair in a population exhibiting
CC the trait with that of a reference population, where the
CC haplotype/haplotype pair is one described in the specification and a
CC higher frequency in the trait population indicates the trait is
CC associated with the haplotype. The sequences and methods of the invention
CC are used to diagnose and develop treatment for disease associated with
CC APOC1 activity, such as hypercholesterolaemia and senile dementia of
CC Alzheimer's type (SDAT). This sequence represents a PCR primer used for
CC detecting human APOC1 DNA polymorphisms
XX
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GGTCACATGG 16
|| |||||||
Db 1 GGCCACATGG 10

RESULT 76
ADG98564
ID ADG98564 standard; DNA; 10 BP.
XX
AC ADG98564;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human CETP gene allele specific extension PCR primer #25.
XX
KW human; cholesteryl ester transfer protein; CETP;
KW single nucleotide polymorphism; SNP; drug screening; atherosclerosis;
KW cardiovascular disease; hypercholesterolaemia;
KW allele specific oligonucleotide; ss; extension PCR; primer.
XX
OS Homo sapiens.
XX
PN WO2003091277-A2.
XX
PD 06-NOV-2003.
XX
PF 28-APR-2003; 2003WO-US013288.
XX
PR 26-APR-2002; 2002US-0375791P.

XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Chew A, Kazemi A, Lachowicz M, Lee HH, Parks KE;
PI Petersen N, Rounds E, Sausker EA, Tirrell C;
XX
DR WPI; 2003-865576/80.
XX
PT New isolated polynucleotide useful for haplotyping and/or genotyping
PT cholesteryl ester transfer protein (CETP) gene in an individual or in
PT screening for drugs useful in treating diseases associated with CETP
PT activity.
XX
PS Claim 45; SEQ ID NO 196; 250pp; English.
XX
CC The invention comprises the amino acid and coding sequences of the human
CC cholesteryl ester transfer protein (CETP), the invention also comprises
CC polymorphisms identified within the CETP gene. The DNA and protein
CC sequences of the invention are useful in haplotyping and/or genotyping
CC the CETP gene in an individual. The DNA and protein sequences may also be
CC used to screen drugs or compounds targeting the CETP or its variant to
CC treat a condition or disease associated with CETP (e.g. atherosclerosis,
CC cardiovascular disease or hypercholesterolaemia). The present DNA
CC sequence represents an allele specific extension PCR primer for the human
CC CETP gene.
XX
SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCATGGTCAC 12
|||||| |||
Db 1 TCATGGACAC 10

RESULT 77
ADQ99469
ID ADQ99469 standard; RNA; 10 BP.
XX
AC ADQ99469;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human CD39L2 gene consensus translation initiation site #2.
XX
KW CD39-like protein; gene mapping; molecular weight marker;
KW food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW NTPase; human; ss.
XX
OS Homo sapiens.
XX
PN US6759214-B1.
XX
PD 06-JUL-2004.
XX
PF 13-JUL-2001; 2001US-00908510.
XX
PR 29-JAN-1999; 99US-00240639.
XX
PA (NUVE-) NUVELO INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2004-515395/49.
XX
PT New CD-39-like polypeptides and polynucleotides, useful in chromosome and
PT gene mapping, as molecular weight markers, as food supplements, or as
PT anti-thrombotic or anti-tissue graft rejection agents.
XX
PS Example; SEQ ID NO 29; 104pp; English.
XX
CC The invention relates to novel CD39-like polypeptides (CD39-like
CC nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding
CC such polypeptides. CD39-like polynucleotides may be used as hybridisation
CC probes, PCR primers and in chromosome and gene mapping. Polypeptides of
CC the invention may be used as molecular weight markers, as food
CC supplements, in generating an antibody that specifically binds the
CC polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or
CC for regulating ATP neurotransmission in smooth muscle, peripheral ganglia
CC or brain. Sequences of the invention are useful in modulating ecto-ATPase
CC activity and for identifying compounds that modulate ecto-ATPase
CC activity. The present sequence is human CD39-like gene consensus
CC translation initiation site. This sequence is used in the exemplification
CC of the invention.
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACATGGATGA 20
||| |||:||
Db 1 ACAAGGAUGA 10

RESULT 78
ADR69198
ID ADR69198 standard; RNA; 10 BP.
XX
AC ADR69198;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human CD39L2 gene consensus translation initiation site #2.
XX
KW CD39-like protein; autoimmune deficiency disorder;
KW connective tissue disease; multiple sclerosis;
KW systemic lupus erythematosus; rheumatoid arthritis;
KW autoimmune pulmonary inflammation; Guillain-Barre syndrome;
KW autoimmune thyroiditis; insulin dependent diabetes mellitus;
KW myasthenia gravis; graft-versus-host disease;
KW autoimmune inflammatory eye disease; allergic disorder; asthma;
KW respiratory disorder; myeloid or lymphoid cell deficiency;
KW periodontal disease; tooth repair process; inflammatory bowel disease;
KW Crohn's disease; leukaemia; nervous system disorder; anticoagulant;
KW food supplement; anti-tissue graft rejection; ATP neurotransmission;
KW gene therapy; human; ss.
XX
OS Homo sapiens.
XX
PN US6780410-B1.
XX
PD 24-AUG-2004.
XX
PF 13-JUL-2001; 2001US-00905744.
XX
PR 29-JAN-1999; 99US-00240639.
XX
PA (NUVE-) NUVELO INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2004-613270/59.
XX
PT New isolated CD39LA polypeptide and polynucleotide, useful for
PT preventing, treating, or ameliorating multiple sclerosis, systemic lupus
PT erythematosus, rheumatoid arthritis, myasthenia gravis, or graft-versus-
PT host disease.
XX
PS Example; SEQ ID NO 29; 103pp; English.
XX
CC The present invention relates to CD39-like polypeptide and its encoding

```
CC   polynucleotide. The invention is useful for preventing, treating or
CC   ameliorating autoimmune deficiency disorders including connective tissue
CC   disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid
CC   arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome,
CC   autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia
CC   gravis, graft-versus-host disease or autoimmune inflammatory eye disease,
CC   allergic disorders including asthma and other respiratory problems,
CC   myeloid or lymphoid cell deficiencies, periodontal diseases and other
CC   tooth repair processes, inflammatory conditions including inflammatory
CC   bowel disease and Crohn's disease, leukaemias and nervous system
CC   disorders. The invention is also useful as an anticoagulant for
CC   inhibiting platelet aggregation, food supplement, anti-tissue graft
CC   rejection agents, for regulating neurotransmission by ATP in smooth
CC   muscle, peripheral ganglia or brain and in gene therapy. The present
CC   sequence is a human CD39L2 gene consensus translation initiation site.
CC   This sequence is used in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  80.0%;  Pred. No. 64;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 79
ADR69032
ID   ADR69032 standard; RNA; 10 BP.
XX
AC   ADR69032;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human CD39L2 gene consensus translation initiation site #2.
XX
KW   CD39-like protein; CD39-like nucleotide triphosphatase; NTPase; cancer;
KW   leukaemia; acute lymphocytic leukaemia; acute myelocytic leukaemia;
KW   chronic leukaemia; autoimmune disorder; multiple sclerosis;
KW   rheumatoid arthritis; Guillain-Barre syndrome;
KW   insulin dependent diabetes mellitus; myasthenia gravis;
KW   graft-versus-host disease; GVHD; allergic disorder; asthma;
KW   respiratory disorder; inflammatory disorder; septic shock;
KW   systemic inflammatory response syndrome; SIRS; Crohn's disease;
KW   central nervous system disorder; peripheral nervous system disorder;
KW   ischaemia; Parkinson's disease; Alzheimer's disease; Huntington's chorea;
KW   systemic lupus erythematosus;
KW   human immunodeficiency virus-associated myelopathy;
KW   transverse myelopathy; nutritional disorder; vitamin B12 deficiency;
KW   folic acid deficiency; Wernicke disease; tobacco-alcohol amblyopia;
KW   Marchiafava-Bignami disease; haemostatic activity; thrombolytic activity;
KW   nutritional supplement; ecto-ATPase activity; cytostatic; immunotherapy;
KW   human; ss.
XX
OS   Homo sapiens.
XX
PN   US6780977-B1.
XX
PD   24-AUG-2004.
XX
PF   27-MAR-2002; 2002US-00107660.
XX
PR   29-JAN-1999;   99US-00240639.
PR   13-JUL-2001; 2001US-00905589.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Chadwick BP,  Frischauf A;
XX
DR   WPI; 2004-613273/59.
XX
PT   New antibody or its fragment that specifically binds to CD39L3
PT   polypeptide, useful for detecting and purifying CD39L3 polypeptide, for
PT   treating leukemia, and for detecting and preventing metastatic spread of
PT   cancerous cells.
XX
PS   Example; Col 57; 102pp; English.
XX
CC   The present invention provides novel CD39-like polypeptides (CD39-like
CC   nucleotide triphosphatase; NTPase) and their encoding polynucleotides.
CC   The invention is useful in treating cancer, leukaemia and related
CC   disorders such as acute lymphocytic leukaemia, acute myelocytic leukaemia
CC   and chronic leukaemia, autoimmune disorders such as multiple sclerosis,
CC   rheumatoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes
CC   mellitus, myasthenia gravis and graft-versus-host disease, allergic
CC   disorders such as asthma, respiratory disorders, inflammatory disorders
CC   such as septic shock, systemic inflammatory response syndrome (SIRS) and
CC   Crohn's disease, central and peripheral nervous system disorders such as
CC   ischaemia, Parkinson's disease, Alzheimer's disease, Huntington's chorea,
CC   systemic lupus erythematosus, human immunodeficiency virus-associated
CC   myelopathy and transverse myelopathy and nutritional disorders such as
CC   vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-
CC   alcohol amblyopia and Marchiafava-Bignami disease. The invention also has
CC   haemostatic and thrombolytic activity, serve as nutritional supplements
CC   and modulates ecto-ATPase activity. The invention acts as a cytostatic
CC   agent and is useful in immunotherapy. The present sequence is human
CC   CD39L2 gene consensus translation initiation site . This sequence is used
CC   in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  80.0%;  Pred. No. 64;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 80
ADR87958/c
ID   ADR87958 standard; DNA; 10 BP.
XX
AC   ADR87958;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Cy3-labelled probe used to detect human NAT-2 wild-type DNA -SEQ ID 136.
XX
KW   SNP detection; drug therapy; probe; ss; human; NAT2;
KW   wild-type N-acetyltransferase 2 isoenzyme.
XX
OS   Homo sapiens.
XX
PN   WO2004069189-A2.
XX
PD   19-AUG-2004.
XX
PF   04-FEB-2004; 2004WO-US002941.
XX
PR   04-FEB-2003; 2003US-0444656P.
XX
PA   (INNO-) INNOVACEUTICALS INC.
XX
PI   Branch RA,  Romkes M;
XX
DR   WPI; 2004-604340/58.
XX
PT   Measuring the expression or activity of a CYP enzyme in a subject by
PT   measuring the expression of the CYP enzyme gene or mRNA expression for
PT   the CYP enzyme in whole blood and normalizing the measured CYP enzyme
PT   gene or mRNA expression.
XX
```

PS Disclosure; SEQ ID NO 136; 73pp; English.
XX
CC The invention relates to a novel method for measuring the expression or
CC activity of a CYP (cytochrome P450), NAT1 (N-acetyltransferase 1) or NAT2
CC (N-acetyltransferase 2) enzyme in a subject comprising measuring the
CC expression of the enzyme gene or mRNA in whole blood and normalising the
CC measured enzyme gene or mRNA expression, respectively. The method may be
CC useful in measuring the expression or activity of an enzyme in a subject
CC and for detecting and quantifying the presence of SNPs (single nucleotide
CC polymorphisms) within an enzyme. Thus, the method of the invention may be
CC utilised in order to predict the effectiveness or safety of a drug
CC therapy, since the drug metabolising capability of an individual is
CC affected by the isoenzymes present within that individual. The current
CC sequence is that of a Cy3-labelled probe which was used to detect human
CC NAT-2 wild-type DNA of the invention.
XX
SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ATGGTCACAT 14
||||||| |
Db 10 ATGGTCACCT 1

RESULT 81
ADS17912
ID ADS17912 standard; RNA; 10 BP.
XX
AC ADS17912;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human CD39L2 gene consensus translation initiation site #2.
XX
KW CD39-like protein; gene mapping; food supplement; ecto-ATPase activity;
KW gene therapy; multiple sclerosis; rheumatoid arthritis;
KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;
KW autoimmune inflammatory eye disease; osteoporosis; osteoarthritis;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW leukaemia; nervous system disorder; neuroprotective; antiarthritic;
KW antirheumatic; antithyroid; immunosuppressive; antidiabetic;
KW muscular-gen; ophthalmological; osteopathic; nootropic; antiparkinsonian;
KW cytostatic; human; ss.
XX
OS Homo sapiens.
XX
PN US6787328-B1.
XX
PD 07-SEP-2004.
XX
PF 13-JUL-2001; 2001US-00905732.
XX
PR 29-JAN-1999; 99US-00240639.
XX
PA (NUVE-) NUVELO INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2004-632929/61.
XX
PT New isolated CD39L4 polynucleotide, useful for preventing, treating, or
PT ameliorating multiple sclerosis, rheumatoid arthritis, diabetes,
PT osteoporosis, Alzheimer's disease, amyotrophic lateral sclerosis, or
PT leukemia.
XX
PS Example; SEQ ID NO 29; 103pp; English.
XX
CC The present invention relates to a CD39-like polypeptides and the
CC encoding polynucleotides. The CD39L4 polynucleotide is useful as
CC hybridisation probes, as primers for PCR, for chromosome or gene mapping,
CC in the recombinant production of protein, and in generation of antisense
CC DNA or RNA. The protein of the invention is used as molecular weight
CC markers, and as food supplements and for modulating ecto-ATPase activity
CC and for identifying compounds that can be utilised for modulating ecto-
CC ATPase activity. The invention is useful for preventing, treating or
CC ameliorating a medical condition, e.g. multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, diabetes mellitus, myasthenia gravis,
CC autoimmune inflammatory eye disease, osteoporosis, osteoarthritis,
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC leukaemia or nervous system disorders and in gene therapy. The present
CC sequence is the human CD39L2 gene consensus translation initiation site.
CC This sequence is used in the exemplification of the invention.
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACATGGATGA 20
||| |||:||
Db 1 ACAAGGAUGA 10

RESULT 82
ADR87808
ID ADR87808 standard; DNA; 10 BP.
XX
AC ADR87808;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human CD39L2 gene consensus translation initiation site #2.
XX
KW CD39-like protein; CD39-like nucleotide-triphosphatase; NTPase;
KW HIV infection; hepatitis; multiple sclerosis;
KW systemic lupus erythematosus; rheumatoid arthritis;
KW Guillain-Barre syndrome; thyroiditis; diabetes; myasthenia gravis;
KW graft-versus-host disease; GHVD; asthma; human; ss.
XX
OS Homo sapiens.
XX
PN US6783959-B1.
XX
PD 31-AUG-2004.
XX
PF 27-MAR-2002; 2002US-00107576.
XX
PR 29-JAN-1999; 99US-00240639.
PR 13-JUL-2001; 2001US-00908510.
XX
PA (NUVE-) NUVELO INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2004-623544/60.
XX
PT New isolated CD39L3 polypeptide and polynucleotide, useful for
PT diagnosing, preventing or treating HIV, hepatitis, multiple sclerosis,
PT systemic lupus erythematosus, arthritis, diabetes and asthma.
XX
PS Example; SEQ ID NO 29; 102pp; English.
XX
CC The invention relates to CD39-like polypeptides (CD39-like nucleotide-
CC triphosphatase; NTPase) and their corresponding polynucleotides. The
CC invention also relates to a method for making CD39L proteins. The methods
CC and compositions of the invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CD39-like polypeptide, such as HIV
CC infection, hepatitis, multiple sclerosis, systemic lupus erythematosus,
CC rheumatoid arthritis, Guillain-Barre syndrome, thyroiditis, diabetes,
CC myasthenia gravis, graft-versus-host disease (GHVD) and asthma. The
CC present sequence is the human CD39L2 gene consensus translation

```
CC   initiation site. This sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 64;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 83
ADV16922
ID   ADV16922 standard; RNA; 10 BP.
XX
AC   ADV16922;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Human CD39L2 consensus translational intiation site #2.
XX
KW   Diagnostic; genetic engineering; immune disorder; immune deficiency;
KW   microbial infection; virucide; antibacterial; fungicide;
KW   autoimmune disorder; immunosuppressive; respiratory disorder;
KW   repiratory gen; antiasthmatic; cancer; cytostatic; immunotherapy;
KW   CD39-like protein; ss; CD39L2.
XX
OS   Homo sapiens.
XX
PN   US6828423-B1.
XX
PD   07-DEC-2004.
XX
PF   13-JUL-2001; 2001US-00905743.
XX
PR   29-JAN-1999;   99US-00240639.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Chadwick BP,  Frischauf A;
XX
DR   WPI; 2005-009982/01.
XX
PT   Isolated antibody or its antigen binding fragment which specifically
PT   binds to a CD39L4 polypeptide, useful for detecting and preventing
PT   metastatic spread of cancerous cells.
XX
PS   Example; SEQ ID NO 29; 104pp; English.
XX
CC   The present invention relates to an antibody or its antigen binding
CC   fragment which specifically binds to a CD39L4 polypeptide. The invention
CC   is useful for treating some forms of cancer, where abnormal expression of
CC   the CD39L4 is involved and for detecting and preventing metastatic spread
CC   of a cancerous cells. The invention is also useful for immuno-affinity
CC   purification of the proteins and to identify cells or tissues in which a
CC   fragment of the CD39L4 polypeptide is expressed. The present sequence is
CC   the human CD39L2 consensus translational intiation site.
XX
SQ   Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 64;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 84
ADZ66991
ID   ADZ66991 standard; RNA; 10 BP.
XX
AC   ADZ66991;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Human CD39L4 RNA intiation site Seq 29.
XX
KW   antibody production; CD39L4; gene mapping; DNA detection; food;
KW   anticoagulant; aggregant; ss.
XX
OS   Homo sapiens.
XX
PN   US6884872-B1.
XX
PD   26-APR-2005.
XX
PF   13-JUL-2001; 2001US-00905589.
XX
PR   29-JAN-1999;   99US-00240639.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Chadwick BP,  Frischauf A;
XX
DR   WPI; 2005-321239/33.
XX
PT   Novel antibody or antigen binding fragment that specifically binds to
PT   CD39L2 polypeptide, useful for detecting CD39L2 polypeptide.
XX
PS   Example; SEQ ID NO 29; 103pp; English.
XX
CC   This invention relates to a novel isolated antibody or antigen-binding
CC   fragment that specifically binds to a human CD39L2 polypeptide comprising
CC   a fully defined 456 amino acid sequence (SEQ ID No:2) as given in the
CC   specification. In particular, it refers to the cloning and
CC   characterization of CD39-like nucleotide triphosphatases (NTPases) and a
CC   hybridoma that produces the monoclonal antibody that can bind to the
CC   CD39L2 protein or an immunologically reactive fragment thereof. The
CC   present invention describes other CD39-like genes that can be used in
CC   various molecular biology techniques including gene mapping and in situ
CC   hybridization for DNA detection. In addition, the encoded CD39-like
CC   proteins can be used as molecular weight markers and as food supplements,
CC   as well as those with ADPase activity are useful as anticoagulants, for
CC   inhibiting platelet aggregation, anti-tissue graft rejection agents and/
CC   or as part of methods for regulating neurotransmission by ATP in smooth
CC   muscle etc. This oligonucleotide is a human CD39L4 RNA initiation site
CC   that shares a poor consensus with the vertebrate consensus site of the
CC   invention.
XX
SQ   Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 64;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10


RESULT 85
ADZ74460
ID   ADZ74460 standard; DNA; 10 BP.
XX
AC   ADZ74460;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Human CD39L2 initiation start site, seq id 29.
XX
KW   Antibacterial; virucide; fungicide; cytostatic; osteopathic;
```

KW immunosuppressive; immunostimulant; vulnerary; antiulcer; dermatological;
KW neuroprotective; nootropic; antiparkinsonian; anticonvulsant; CNS-Gen.;
KW hypertensive; cerebroprotective; vasotropic; antiinfertility; hemostatic;
KW thrombolytic; antiinflammatory; infection; cancer; degeneration;
KW endocrine disease; musculoskeletal disease; immune disorder; injury;
KW neurological disease; cardiovascular disease; ds.
XX
OS Homo sapiens.
XX
PN US6899875-B1.
XX
PD 31-MAY-2005.
XX
PF 27-MAR-2002; 2002US-00108171.
XX
PR 29-JAN-1999; 99US-00240639.
PR 13-JUL-2001; 2001US-00905743.
XX
PA (NUVE-) NUVELO INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2005-381494/39.
XX
PT New CD39L3 polypeptide having phosphohydrolase activity, useful in
PT preparing a composition for treating e.g., bacterial, viral or fungal
PT infection, cancer, osteoporosis or autoimmune disorders.
XX
PS Example; SEQ ID NO 29; 103pp; English.
XX
CC The invention relates to a new isolated CD39L3 polypeptide, having
CC phosphohydrolase activity, and comprising a 529-amino acid sequence,
CC fully defined in the specification ADZ74435. The polypeptide is useful in
CC preparing a composition for treating disorders or diseases, e.g.,
CC bacterial, viral or fungal infection, cancer, osteoporosis or autoimmune
CC disorders, or can be used to stimulate immune function. They may also be
CC useful for wound healing and tissue repair and replacement, and in the
CC treatment of burns, incisions and ulcers. They may be used in the
CC treatment of diseases of the peripheral nervous system, such as
CC peripheral nerve injuries, peripheral neuropathy and localized
CC neuropathies, and central nervous system diseases, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis,
CC and Shy Drager syndrome. They are also useful in the treatment of spinal
CC cord disorders and stroke. The protein may be useful as a fertility
CC inducing therapeutic. The polypeptide may also exhibit hemostatic or
CC thrombolytic activity, and antiinflammatory activity. The purified
CC polypeptides can be used in in vitro binding assays to identify molecules
CC which bind to the polypeptides. The polypeptides can be used in a panel
CC of multiple proteins for high-throughput screening, to raise antibodies
CC or to elicit another immune response, as a reagent (including the labeled
CC reagent) in assays designed to quantitatively determine levels of the
CC protein (or its receptor) in biological fluids, as markers for tissues in
CC which the corresponding protein is preferentially expressed, and to
CC isolate correlative receptors or ligands. They can also be used as
CC nutritional sources or supplements. The current sequence represents a
CC possible human CD39L2 initiation start site containing fragment.
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 64;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| |||:||
Db          1 ACAAGGAUGA 10
```

RESULT 86
ABQ86788
ID ABQ86788 standard; cDNA; 11 BP.
XX
AC ABQ86788;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 543.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 59; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db          2 CTCGTGGTCA 11
```

RESULT 87
ABV63400
ID ABV63400 standard; cDNA; 11 BP.
XX
AC ABV63400;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1186.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.

XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 57; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db          2 CTCGTGGTCA 11
```

RESULT 88
ABV65674/c
ID ABV65674 standard; cDNA; 11 BP.
XX
AC ABV65674;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3460.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 121; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACAT 14
              |||||| |||
Db         11 ATGGTCCCAT 2
```

RESULT 89
ABV64959/c
ID ABV64959 standard; cDNA; 11 BP.
XX
AC ABV64959;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2745.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 101; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag

```
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 TCACATGGAT 18
              ||||| ||||
Db         10 TCACAGGGAT 1


RESULT 90
ABV70821
ID   ABV70821 standard; cDNA; 11 BP.
XX
AC   ABV70821;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8607.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 275; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db          2 CTCGTGGTCA 11


RESULT 91
ACC58070
ID   ACC58070 standard; DNA; 11 BP.
XX
AC   ACC58070;
XX
DT   11-AUG-2003  (first entry)
XX
DE   DNA helper probe hj-DNA 11'mer as 5' end.
XX
KW   Nucleic acid detection; SNP; single nucleotide polymorphism; genotyping;
KW   probe; ss.
XX
OS   Synthetic.
XX
PN   EP1251183-A2.
XX
PD   23-OCT-2002.
XX
PF   18-FEB-2002; 2002EP-00388014.
XX
PR   18-APR-2001; 2001US-0284729P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Jacobsen N,  Jakobsen MH,  Skouv J;
XX
DR   WPI; 2003-459558/44.
XX
PT   Detecting a nucleotide target sequence for detecting genetic disease, by
PT   using a helper probe.
XX
PS   Example 1; Page 11; 24pp; English.
XX
CC   The present sequence is that of a DNA helper probe, designated hj-DNA
CC   11'mer as 5' end. This helper probe was used in an example from the
CC   invention in which linked nucleic acid (LNA) helper probes were used to
CC   improve the capture of single-stranded DNA targets by immobilised
CC   anthraquinone-coupled LNA capture probes. This is an example of a method
CC   for enhancing hybridisation of a capture oligonucleotide to a target
CC   sequence using a helper probe comprising modified nucleotide residues.
CC   The method exhibits significantly improved binding abilities, and is
CC   particularly suited for detection of single nucleotide polymorphism
CC   sites, for genotyping and diagnosis of genetic disease
XX
SQ   Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||||||| ||
Db          1 ACATGGAGGA 10


RESULT 92
ACC58066
ID   ACC58066 standard; DNA; 11 BP.
XX
AC   ACC58066;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Linked nucleic acid helper probe hj-LNA 11'mer as 5' end.
XX
KW   Locked nucleic acid; LNA; nucleic acid detection; SNP;
KW   single nucleotide polymorphism; genotyping; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .11
```

```
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= linked nucleic acids"
FT   modified_base   2
FT                   /*tag= b
FT                   /mod_base= m5c
FT                   /note= "5-methylcytidine"
FT   modified_base   11
FT                   /*tag= c
FT                   /mod_base= m5c
FT                   /note= "5-methylcytidine"
XX
PN   EP1251183-A2.
XX
PD   23-OCT-2002.
XX
PF   18-FEB-2002; 2002EP-00388014.
XX
PR   18-APR-2001; 2001US-0284729P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Jacobsen N,  Jakobsen MH,  Skouv J;
XX
DR   WPI; 2003-459558/44.
XX
PT   Detecting a nucleotide target sequence for detecting genetic disease, by
PT   using a helper probe.
XX
PS   Example 1; Page 10; 24pp; English.
XX
CC   The present sequence is that of a linked nucleic acid (LNA) helper probe,
CC   designated hj-LNA 11'mer as 5' end. This helper probe was used in an
CC   example from the invention in which LNA helper probes were used to
CC   improve the capture of single-stranded DNA targets by immobilised
CC   anthraquinone-coupled LNA capture probes. This is an example of a method
CC   for enhancing hybridisation of a capture oligonucleotide to a target
CC   sequence using a helper probe comprising modified nucleotide residues.
CC   The method exhibits significantly improved binding abilities, and is
CC   particularly suited for detection of single nucleotide polymorphism
CC   sites, for genotyping and diagnosis of genetic disease
XX
SQ   Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 ACATGGATGA 20
               ||||||| ||
Db           1 ACATGGAGGA 10


RESULT 93
ADQ32820/c
ID   ADQ32820 standard; DNA; 11 BP.
XX
AC   ADQ32820;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 910.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 5; SEQ ID NO 910; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           5 ATGGTCACAT 14
                ||||| |||
Db          11 ATGGTCCCAT 2


RESULT 94
ADQ32644
ID   ADQ32644 standard; DNA; 11 BP.
XX
AC   ADQ32644;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 734.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
```

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XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 5; SEQ ID NO 734; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 5 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db          2 ATATGGATGA 11


RESULT 95
ADQ32669/c
ID   ADQ32669 standard; DNA; 11 BP.
XX
AC   ADQ32669;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 759.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 5; SEQ ID NO 759; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              || |||||||
Db         10 CAGATGGATG 1


RESULT 96
ADZ23298
ID   ADZ23298 standard; DNA; 11 BP.
XX
AC   ADZ23298;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human SNP detection related oligonucelotide #265.
XX
KW   ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
KW   immune disorder; cardiovascular disease; metabolic disorder;
KW   respiratory disease; musculoskeletal disease; renal disease;
KW   nephrotropic; endocrine disease; genitourinary disease.
XX
OS   Homo sapiens.
XX
PN   WO2005030952-A1.
XX
PD   07-APR-2005.
XX
PF   30-SEP-2004; 2004WO-JP014784.
XX
PR   30-SEP-2003; 2003JP-00342519.
PR   28-MAY-2004; 2004JP-00158717.
XX
PA   (RIKE ) RIKEN KK.
PA   (STAG-) STAGEN CO LTD.
PA   (SEKI/) SEKINE A.
PA   (IIDA/) IIDA A.
PA   (SAIT/) SAITO S.
XX
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PI   Sekine A,  Iida A,  Saito S,  Nakamura Y,  Kamatani N;
XX
DR   WPI; 2005-305936/31.
XX
PT   Analyzing haplotype, by detecting polymorphism in drug-related genes,
PT   electing common polymorphism (CP), building haplotype block using CP,
PT   specifying CP within block, specifying tag polymorphism from CP within
PT   block.
XX
PS   Disclosure; SEQ ID NO 265; 1290pp; Japanese.
XX
CC   The invention relates to a method of analyzing haplotype, by detecting
CC   gene polymorphism in drug-related genes such as aryl acetylamide
CC   deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
CC   sub-family A (ABC1), member 1. The method is useful for analyzing
CC   haplotype. The method is useful for estimating the sensitivity or disease
CC   of a medicine or a foreign material, for selecting medicine for
CC   preventing or treating diseases, for determining appropriate dosage of
CC   medicine for preventing or treating a disease, for analyzing a drug
CC   interaction, and for determining the related polymorphism relative to the
CC   sensitivity of the medicine, foreign material or disease. The diseases
CC   include malignant tumor, immune disorder circulatory disease, metabolic
CC   disease, kidney disease, respiratory disease and muscle associated
CC   disease. The method enables analysis of the individual differences
CC   related to the sensitivity of a medicine, using a haplotype, without
CC   using each single nucleotide polymorphism. The present sequence
CC   represents a human SNP detection related oligonucelotide.
XX
SQ   Sequence 11 BP; 4 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 72;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||||| ||||
Db          2 CTCATAGTCA 11


RESULT 97
AAQ24034
ID   AAQ24034 standard; DNA; 12 BP.
XX
AC   AAQ24034;
XX
DT   25-MAR-2003  (revised)
DT   21-SEP-1992  (first entry)
XX
DE   Herpesvirus inhibiting antisense oligonucleotide.
XX
KW   HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
KW   Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
XX
OS   Synthetic.
XX
PN   WO9205284-A.
XX
PD   02-APR-1992.
XX
PF   18-SEP-1991;   91WO-US006646.
XX
PR   21-SEP-1990;   90US-00586185.
XX
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Aurelian L,  Tso P;
XX
DR   WPI; 1992-132145/16.
XX
PT   New anti:sense oligo:nucleotide(s) for inhibiting HSV - also used for
PT   diagnosis and for inhibiting HIV activation by herpes virus.
XX
PS   Claim 1; Page 38; 77pp; English.
XX
CC   The sequence is that of an antisense oligonucleotide which can be used
CC   for inhibiting growth or replication of herpesviruses. It corresponds to
CC   an antisense sequence of a herpesvirus site, pref. in a gene that is
CC   essential for synthesising nucleic acids e.g. the immediate early genes
CC   or Vmw65. It can be prepd. by solid phase triester or phosphor- amidite
CC   chemistry or by recombinant DNA techniques. It can be used for treating
CC   infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
CC   (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
CC   (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
CC   inhibition of herpesvirus growth or replication may indirectly forestall
CC   the progression of events from HIV exposure to the clinical manifestation
CC   of AIDS. It may also be useful in the detection, diagnosis and
CC   manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
CC   Q24044. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 12 BP; 5 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACA 13
              |||||| |||
Db          2 CATGGTAACA 11


RESULT 98
AAQ30497/c
ID   AAQ30497 standard; DNA; 12 BP.
XX
AC   AAQ30497;
XX
DT   25-MAR-2003  (revised)
DT   19-MAR-1993  (first entry)
XX
DE   Adenovirus major late transcription factor element under control of TCRE.
XX
KW   Transcriptional control recognition element; decoy; cellular RNA;
KW   promoter; hormone receptor element; viral; liver; tissue; viral;
KW   proliferation; linker; NF-1; ss.
XX
OS   Synthetic.
XX
PN   WO9218522-A1.
XX
PD   29-OCT-1992.
XX
PF   17-APR-1992;   92WO-US003205.
XX
PR   18-APR-1991;   91US-00687337.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Chu BC,  Orgel L;
XX
DR   WPI; 1992-382035/46.
XX
PT   New oligo-nucleotide(s) contg. transcription control recognition element
PT   - stabilised by covalent bonding of two DNA strands, act as decoys for
PT   regulatory protein to modulate specific RNA.
XX
PS   Disclosure; Page 6; 41pp; English.
XX
CC   Transcriptional control recognition element recognition sequences may be
CC   recognised by control proteins and are involved in either enhancing or
CC   repressing transcription of associated sequences. TCR sequences include
CC   promoter elements, hormone receptor elements, viral, cellular, liver or
CC   tissue elements, etc. The sequence represents an exemplary viral and
CC   cellular element, the adenovirus major late transcription factor. A
CC   typical application of the TCRE recognising oligonucleotides is
CC   inhibition of viral proliferation. See also AAQ30472-518. (Updated on 25-
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CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 99
AAQ52946/c
ID   AAQ52946 standard; RNA; 12 BP.
XX
AC   AAQ52946;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   Herpes simplex virus target sequence 24.
XX
KW   RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
KW   picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KW   papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
KW   T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KW   influenza virus; HSV; herpes simplex virus; vector; immune response;
KW   antibody; ribozyme; viral RNA; treatment; ss.
XX
OS   Synthetic.
XX
PN   WO9323569-A1.
XX
PD   25-NOV-1993.
XX
PF   29-APR-1993;   93WO-US004020.
XX
PR   11-MAY-1992;   92US-00882689.
PR   14-MAY-1992;   92US-00882712.
PR   14-MAY-1992;   92US-00882713.
PR   14-MAY-1992;   92US-00882714.
PR   14-MAY-1992;   92US-00882823.
PR   14-MAY-1992;   92US-00882824.
PR   14-MAY-1992;   92US-00882886.
PR   14-MAY-1992;   92US-00882888.
PR   14-MAY-1992;   92US-00882889.
PR   14-MAY-1992;   92US-00882921.
PR   14-MAY-1992;   92US-00882922.
PR   14-MAY-1992;   92US-00883823.
PR   14-MAY-1992;   92US-00883849.
PR   14-MAY-1992;   92US-00884073.
PR   14-MAY-1992;   92US-00884074.
PR   14-MAY-1992;   92US-00884333.
PR   14-MAY-1992;   92US-00884422.
PR   14-MAY-1992;   92US-00884431.
PR   14-MAY-1992;   92US-00884436.
PR   14-MAY-1992;   92US-00884521.
PR   31-JUL-1992;   92US-00923738.
PR   26-AUG-1992;   92US-00935854.
PR   26-AUG-1992;   92US-00936086.
PR   18-SEP-1992;   92US-00948359.
PR   15-OCT-1992;   92US-00963322.
PR   07-DEC-1992;   92US-00987129.
PR   07-DEC-1992;   92US-00987130.
PR   07-DEC-1992;   92US-00987133.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Draper KG,  Dudycz LW,  Mcswiggen JA,  Macejak DG,  Holecek JJ;
PI   Mamone JA;
XX
DR   WPI; 1993-386599/48.
XX
PT   Enzymatic RNA molecules - used to inhibit viral replication, infection
PT   and gene expression.
XX
PS   Claim 5; Fig 15; 287pp; English.
XX
CC   The sequences (AAQ52923-Q53037) are pref. herpes simplex virus target
CC   sequences for enzymatic RNA molecules. The RNA molecules are
CC   complementary to a substrate binding region in the specified gene target.
CC   They also have enzymatic activity, in that they specifically cleave RNA
CC   in the target. The ERMs interfere with viral replication and therefore
CC   have anti-viral properties. They can be used to attenuate viruses to be
CC   used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
CC   PI field.)
XX
SQ   Sequence 12 BP; 2 A; 4 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 100
AAZ59958/c
ID   AAZ59958 standard; DNA; 12 BP.
XX
AC   AAZ59958;
XX
DT   19-APR-2000  (first entry)
XX
DE   Adenovirus Ad5 major late promoter (MLP) upstream promoter element (UPE).
XX
KW   Major late promoter; MLP; mutation; upstream promoter element; UPE;
KW   recombinant adenovirus; E1 region deficiency; gene therapy;
KW   replication incompetent; ds.
XX
OS   Mastadenovirus.
XX
PN   WO200000628-A1.
XX
PD   06-JAN-2000.
XX
PF   24-JUN-1999;   99WO-US014333.
XX
PR   26-JUN-1998;   98US-00105515.
XX
PA   (GENV-) GENVEC INC.
XX
PI   Brough DE,  Kovesdi I;
XX
DR   WPI; 2000-147271/13.
XX
PT   Novel replication-defective adenoviruses with a mutated major late
PT   promoter used to study viral molecular genetics and as viral vectors for
PT   genetic transfer.
XX
PS   Disclosure; Page 18; 23pp; English.
XX
CC   The invention relates to a recombinant adenovirus comprising a genome
CC   with a deficiency in the E1 region and a mutation in the major late
CC   promoter (MLP), so that the MLP is less active within a cell other than a
CC   packaging cell. The recombinant adenoviruses are highly useful in
CC   biological research. They can be used to study viral molecular genetics
CC   and cytotoxicity, and to investigate the cell biology of viral growth and
CC   infection. They can also be used to investigate molecular and cellular
CC   biology of gene expression and regulation in novel genetic backgrounds,
CC   e.g., interaction of gene products, ability of transcription factors to
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CC   transregulate gene expression via promoter, or enhancer elements
CC   engineered into the adenovirus. The adenoviruses are also useful as gene
CC   transfer vehicles, e.g., to introduce transgenes into tissues or cells,
CC   and may thus be used as gene therapy vectors. The recombinant
CC   adenoviruses can be grown without the presence of DNA complementary to
CC   the wild type adenoviral MLP, substantially reducing the probability for
CC   generating replication competent adenovirus (RCA). In addition, because
CC   the viruses have a MLP which greatly attenuates L1-L5 gene expression in
CC   nonpermissive host cells, they are less able than first generation
CC   vectors to express late viral gene products in a host cell. Sequences
CC   AAZ59957-Z59960 represent promoter elements of the MLP of adenovirus
CC   serotype 5 (Ad5). The present sequence represents the upstream promoter
CC   element (UPE), which is located 63 bp upstream of the transcriptional
CC   start site
XX
SQ   Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 101
AAA30866
ID   AAA30866 standard; DNA; 12 BP.
XX
AC   AAA30866;
XX
DT   19-SEP-2000  (first entry)
XX
DE   Fragment of a plasmid for expressing a ubiquitin monomer.
XX
KW   Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;
KW   plasmid fragment; ss.
XX
OS   Unidentified.
XX
PN   WO200036129-A1.
XX
PD   22-JUN-2000.
XX
PF   11-DEC-1998;   98WO-SG000103.
XX
PR   11-DEC-1998;   98WO-SG000103.
XX
PA   (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
PI   Fang R,  Wu J,  Chen X;
XX
DR   WPI; 2000-431604/37.
XX
PT   Production of desired protein in plants or plant cells by linking a
PT   ubiquitin monomer coding sequence upstream of the gene encoding the
PT   desired protein.
XX
PS   Example 2; Page 20; 42pp; English.
XX
CC   This sequence represents a fragment of a plasmid expressing a fusion
CC   construct encoding a fusion protein having a ubiquitin monomer linked to
CC   a protein of interest. The invention relates to a method for enhancing
CC   production of a desired protein in a plant or plant cell by inserting a
CC   nucleic acid (NA) encoding a ubiquitin monomer upstream of a NA encoding
CC   the desired protein, where the fusion construct encodes a fusion protein
CC   and expression is not controlled by the ubiquitin promoter. The invention
CC   also relates to a NA acid vector a NA vector able to transform a plant
CC   cell, that comprises NA encoding a fusion protein having a ubiquitin
CC   monomer linked to a protein of interest and further, where expression of
CC   the fusion construct is not under control of a ubiquitin promoter. The
CC   construct allows enhanced production of the desired protein in plants or
CC   plant cells
XX
SQ   Sequence 12 BP; 3 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGA 17
              ||| ||||||
Db          2 GTCGCATGGA 11


RESULT 102
ABI48155/c
ID   ABI48155 standard; DNA; 12 BP.
XX
AC   ABI48155;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 348128 for detecting SNP TSC0045459.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 348128; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db         12 AGATGGATGA 3
```

```
RESULT 103
ABI35107
ID   ABI35107 standard; DNA; 12 BP.
XX
AC   ABI35107;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 335080 for detecting SNP TSC0038590.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 335080; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db          2 AAATGGATGA 11


RESULT 104
ABI72389
ID   ABI72389 standard; DNA; 12 BP.
XX
AC   ABI72389;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 372362 for detecting SNP TSC0059339.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 372362; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db          2 ATATGGATGA 11


RESULT 105
ABH84083/c
ID   ABH84083 standard; DNA; 12 BP.
XX
AC   ABH84083;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 284076 for detecting SNP TSC0011646.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
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```
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 284076; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity  90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db         11 ATATGGATGA 2


RESULT 106
ABI04761
ID   ABI04761 standard; DNA; 12 BP.
XX
AC   ABI04761;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 304734 for detecting SNP TSC0021079.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 304734; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity  90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              || ||||||||
Db          2 ACGTGGATGA 11


RESULT 107
ABH67680
ID   ABH67680 standard; DNA; 12 BP.
XX
AC   ABH67680;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 267657 for detecting SNP TSC0000420.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 267657; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 12;
```

```
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db          1 ATATGGATGA 10


RESULT 108
ABI08303/c
ID   ABI08303 standard; DNA; 12 BP.
XX
AC   ABI08303;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 308276 for detecting SNP TSC0022938.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 308276; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              || |||||||
Db         12 ACGTGGATGA 3


RESULT 109
ABI29750/c
ID   ABI29750 standard; DNA; 12 BP.
XX
AC   ABI29750;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 329723 for detecting SNP TSC0035111.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 329723; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db         11 AAATGGATGA 2


RESULT 110
AAH49257
ID   AAH49257 standard; DNA; 12 BP.
XX
AC   AAH49257;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #20.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
PN   EP1113021-A2.
```

```
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 43; Page 46; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 111
AAH49256
ID   AAH49256 standard; DNA; 12 BP.
XX
AC   AAH49256;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #19.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 43; Page 46; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
```

```
                  | ||||||||
Db          2 CATCATGGTC 11

RESULT 112
AAH49260
ID   AAH49260 standard; DNA; 12 BP.
XX
AC   AAH49260;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #23.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 43; Page 46; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
                | ||||||||
Db          2 CATCATGGTC 11


RESULT 113
AAH49261
ID   AAH49261 standard; DNA; 12 BP.
XX
AC   AAH49261;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #24.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 43; Page 46; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
```

```
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes; (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 114
AAH49259
ID   AAH49259 standard; DNA; 12 BP.
XX
AC   AAH49259;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #22.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 43; Page 46; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 115
AAH49258
ID   AAH49258 standard; DNA; 12 BP.
XX
AC   AAH49258;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #21.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 43; Page 46; 54pp; German.
```

```
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 116
ABA82718/c
ID   ABA82718 standard; DNA; 12 BP.
XX
AC   ABA82718;
XX
DT   07-FEB-2002  (first entry)
XX
DE   Human protective DNA sequence CNI-00735 fragment #4.
XX
KW   Human; protective sequence; cell death; cancer; autoimmune disease;
KW   neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200176457-A2.
XX
PD   18-OCT-2001.
XX
PF   09-APR-2001; 2001WO-US011663.
XX
PR   11-APR-2000; 2000US-00547735.
XX
PA   (COGE-) COGENT NEUROSCIENCE INC.
XX
PI   Thomas MB,  Portbury SD,  Puranam K,  Katz LC,  Lo DC,  Barney S;
XX
DR   WPI; 2002-025874/03.
XX
PT   New protective sequences and their products, useful for diagnosing and
PT   treating diseases involving cell death, including neurological disorders
PT   e.g. stroke and for identifying modulators of expression of the
PT   protective sequences.
XX
PS   Claim 2; Fig 5; 283pp; English.
XX
CC   The present invention relates to protective sequence proteins (ABB44624-
CC   ABB44830) and their coding sequences (ABA82701-ABA82937). The sequences,
CC   when introduced into a cell either predisposed to undergo cell death or
CC   in the process of undergoing cell death, prevent, delay or rescue the
CC   cell from death, hence, these sequences are named "protective sequences".
CC   The sequences are useful for treating and/or ameliorating cancer,
CC   autoimmune diseases and neurological disorders e.g. stroke. Further
CC   examples of diseases which may be treated by the present invention are
CC   given in the specification
XX
SQ   Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              | ||||||||
Db         11 CACATGGTCA 2


RESULT 117
ABK72560
ID   ABK72560 standard; DNA; 12 BP.
XX
AC   ABK72560;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Human OPA1 gene, exon/intron junction #27.
XX
KW   Human; ophthalmological; OPA1; autosomal dominant optic atrophy; ADOA;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200227022-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-GB004284.
XX
PR   26-SEP-2000; 2000GB-00023555.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (UYEY-) UNIV EYE HOSPITAL.
XX
PI   Bhattacharya S,  Wissinger B,  Alexander C,  Votruba M;
XX
DR   WPI; 2002-416484/44.
XX
PT   Novel human normal or mutant OPA1 (the predominant locus for autosomal
PT   dominant optic atrophy (ADOA)) polypeptides and the OPA1 gene, useful in
PT   the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
XX
PS   Disclosure; Fig 12; 75pp; English.
XX
CC   The invention relates to an isolated human normal or mutant OPA1 (the
CC   predominant locus for autosomal dominant optic atrophy (ADOA))
CC   polypeptide (I), characterised by a molecular weight of about 112 kDa,
CC   and substantially free of other human proteins. Also described is the DNA
```

```
CC   (II) encoding (I). (I) and (II) are useful as a medicament, for the
CC   treatment of a medical condition resulting from a defect in the OPA1
CC   gene, which results in autosomal dominant optic atrophy. The nucleic acid
CC   and antibodies to (I) are useful in a variety of hybridisation and
CC   immunological assays to screen for, and to detect the presence of, either
CC   a normal or a defective OPA1 gene or gene product. ABK72533-ABK72593
CC   represent the human OPA1 gene and intron/exon splice junctions
XX
SQ   Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 TCACATGGAT 18
              ||| ||||||
Db          3 TCAGATGGAT 12


RESULT 118
ABA01332/c
ID   ABA01332 standard; RNA; 12 BP.
XX
AC   ABA01332;
XX
DT   29-AUG-2003  (revised)
DT   03-JUL-2002  (first entry)
XX
DE   HIV-1 rev oligonucleotide #5.
XX
KW   Selenoprotein; HIV; Ebola virus; cancer; immune system disorder; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   US6303295-B1.
XX
PD   16-OCT-2001.
XX
PF   12-JUL-1996;   96US-00679493.
XX
PR   14-JUL-1995;   95US-0001203P.
PR   01-SEP-1995;   95US-0003112P.
XX
PA   (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI   Taylor EW,  Nadimpalli RG,  Ramanathan CS;
XX
DR   WPI; 2002-024734/03.
XX
PT   New selenoprotein for use in detecting certain viruses, e.g. human
PT   immunodeficiency virus (HIV) or Ebola, cancer and immune system
PT   disorders.
XX
PS   Disclosure; Col 26; 140pp; English.
XX
CC   The present invention relates to selenoproteins encoded in the genome of
CC   a virus, where the coding sequence of the selenoprotein is genetically
CC   engineered for expression in a nucleic acid construct. The invention also
CC   discloses a method for identifying selenoprotein coding sequences, for
CC   detecting certain viruses (e.g. HIV or Ebola), cancer and immune system
CC   disorders. The present sequence was used to illustrate the invention.
CC   (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 12 BP; 4 A; 3 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         11 CTCAGGGTCA 2


RESULT 119
AAK98610
ID   AAK98610 standard; DNA; 12 BP.
XX
AC   AAK98610;
XX
DT   16-APR-2002  (first entry)
XX
DE   Modified peptide nucleic acid #1.
XX
KW   Peptide nucleic acid; PNA; polyamide backbone; phosphoryl radical;
KW   cytostatic; virucide; dermatological; antiasthmatic; cancer; antisense;
KW   viral infection; vitiligo; pigmentation disorder; asthma; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "modified by phosphate and N-(2-
FT                    hydroxyethyl)glycine"
FT   modified_base    12
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "modified by hex"
XX
PN   WO200179249-A2.
XX
PD   25-OCT-2001.
XX
PF   07-APR-2001; 2001WO-EP004027.
XX
PR   18-APR-2000; 2000DE-01019136.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G,  Will DW;
XX
DR   WPI; 2002-089643/12.
XX
PT   New peptide nucleic acid derivatives, useful e.g. for treating tumors and
PT   diagnosis, have N-terminal phosphoryl residue for improving e.g.
PT   solubility in water.
XX
PS   Example 3; Page 38; 96pp; German.
XX
CC   The present invention relates to peptide nucleic acid (PNA) derivatives.
CC   These can be used in the treatment of cancer, viral infections, vitiligo
CC   or other pigmentation disorders, and asthma. The present sequence is an
CC   oligonucleotide fragment of a PNA described in the exemplification of the
CC   invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 120
ABA97503
ID   ABA97503 standard; DNA; 12 BP.
XX
AC   ABA97503;
XX
DT   16-APR-2002  (first entry)
XX
```

DE Peptide nucleic acid SEQ ID NO: 50.
XX
KW Peptide nucleic acid; PNA; polyamide backbone; phosphoryl radical;
KW cytostatic; virucide; dermatological; antiasthmatic; cancer; antisense;
KW viral infection; vitiligo; pigmentation disorder; asthma; ss.
XX
OS Synthetic.
XX
PN WO200179249-A2.
XX
PD 25-OCT-2001.
XX
PF 07-APR-2001; 2001WO-EP004027.
XX
PR 18-APR-2000; 2000DE-01019136.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G, Will DW;
XX
DR WPI; 2002-089643/12.
XX
PT New peptide nucleic acid derivatives, useful e.g. for treating tumors and
PT diagnosis, have N-terminal phosphoryl residue for improving e.g.
PT solubility in water.
XX
PS Disclosure; Page 91; 96pp; German.
XX
CC The present invention relates to peptide nucleic acid (PNA) derivatives.
CC These can be used in the treatment of cancer, viral infections, vitiligo
CC or other pigmentation disorders, and asthma. The present sequence is an
CC oligonucleotide fragment of a PNA described in the exemplification of the
CC invention
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCATGGTC 10
|||||||||
Db 2 CATCATGGTC 11

RESULT 121
ADM56294/c
ID ADM56294 standard; DNA; 12 BP.
XX
AC ADM56294;
XX
DT 03-JUN-2004 (first entry)
XX
DE Mouse SLC26A6 anion transporter protein gene splice site #13.
XX
KW SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;
KW splice site; ds; mouse; murine.
XX
OS Mus musculus.
XX
PN WO2003072759-A2.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006469.
XX
PR 28-FEB-2002; 2002US-0360275P.
XX
PA (UYVA-) UNIV VANDERBILT.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Mount DB, Romero MF;
XX
DR WPI; 2003-712726/67.
XX
PT New SLC26A6, SLC26A1 or SLC26A2 polypeptide, useful for preparing a
PT composition for treating e.g., cancer.
XX
PS Example 2; SEQ ID NO 26; 204pp; English.
XX
CC The invention comprises the amino acid and coding sequences of SLC26A6,
CC SLC26A1 and SLC26A2 anion transporter proteins. The DNA and protein
CC sequences of the invention are useful for treating cancer. The present
CC DNA sequence represents a splice site from the gene encoding the mouse
CC SLC26A6 anion transporter protein.
XX
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCACATGGAT 18
||||||.|||
Db 10 TCACATAGAT 1

RESULT 122
ADQ29965
ID ADQ29965 standard; DNA; 12 BP.
XX
AC ADQ29965;
XX
DT 09-SEP-2004 (first entry)
XX
DE Rat VR1 exon 1d transcription factor binding fragment #41.
XX
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;
KW detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;
KW hypalgesia; hyperalgesia; neuralgia; myalgia; rat.
XX
OS Rattus sp.
XX
PN WO2004053120-A2.
XX
PD 24-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-EP013522.
XX
PR 09-DEC-2002; 2002DE-01057421.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Weihe E, Bieller A, Schaefer MKH;
XX
DR WPI; 2004-468868/44.
XX
PT New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX
PS Disclosure; Page 46; 68pp; German.
XX
CC This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VR1
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridises to it under
CC standard conditions. The VR1 modulator is derived from one or more of
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VR1 modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VR1 receptor by introducing the

```
CC   modulator or the vector into a cell that contains the VR1 gene. The
CC   products of the invention are used for detecting a transcription factor
CC   from its binding to a regulatory sequence (or a double-stranded
CC   oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC   linked immunosorbant assay, particularly for diagnosis of diseases
CC   associated with overexpression or underexpression of the transcription
CC   factor. The region that modulates VR1 receptor expression includes a
CC   binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or
CC   GATA1. The nucleic acids of the invention, or vectors containing them,
CC   are used for prevention or treatment of pain, also for treating
CC   sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC   neuralgia and myalgia, that are associated with activity of the VR1
CC   receptor. This sequence represents a fragment of rat VR1 exon 1d DNA
CC   which is capable of binding to a transcription factor.
XX
SQ   Sequence 12 BP; 3 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
               |||| |||||
Db          1 CACAGGGATG 10


RESULT 123
AEF80873/c
ID   AEF80873 standard; DNA; 12 BP.
XX
AC   AEF80873;
XX
DT   20-APR-2006  (first entry)
XX
DE   MLTF/USF promoter target DNA fragment.
XX
KW   Gene expression; gene regulation; platinum zinc complex; cancer; tumor;
KW   neoplasm; promoter; target; ds.
XX
OS   Unidentified.
XX
PN   JP2006045131-A.
XX
PD   16-FEB-2006.
XX
PF   05-AUG-2004; 2004JP-00229182.
XX
PR   05-AUG-2004; 2004JP-00229182.
XX
PA   (UYTK ) UNIV TOKYO RIKA GH.
XX
PI   Aoki S,  Okaya R,  Takeda T,  Kimura E;
XX
DR   WPI; 2006-150505/16.
XX
PT   Novel platinum-zinc complex useful as agent for controlling expression of
PT   promoter sequence or RNA of specific gene for treatment of cancer.
XX
PS   Example 4; Page 10; 21pp; Japanese.
XX
CC   The invention relates to a novel platinum-zinc complex (C1) used in the
CC   regulation of gene expression. The complex of the invention is prepared
CC   by reacting a 2,2'-bipyridyl derivative and a cyclen derivative protected
CC   by t-butoxycarbonyl (Boc), adding the platinum compound to the obtained
CC   complex. (C1) is useful as an agent for controlling the expression of a
CC   specific gene. This involves contacting (C1) with the nucleic acid
CC   sequence of the gene, where the nucleic acid sequence is a promoter
CC   sequence which controls the expression of the gene, or an RNA encoding
CC   the gene. The platinum complex in (C1) has increased anti-tumor activity
CC   with respect to solid tumors such as testicular tumors, ovarian cancer,
CC   head and neck cancer, esophageal cancer and small cell lung carcinoma.
CC   (C1) controls the gene expression by the combination of zinc and platinum
CC   complex in its structure. The current sequence represents a promoter
CC   fragment that may act as a target for the complex of the invention.
XX
SQ   Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
                |||||| |||
Db         12 GGTCACGTGG 3


RESULT 124
AAV63047/c
ID   AAV63047 standard; RNA; 8 BP.
XX
AC   AAV63047;
XX
DT   15-JAN-1999  (first entry)
XX
DE   Synthetic RNA 8mer oligonucleotide primer.
XX
KW   Sequencing; biopolymer; mass spectrometry; nuclease; peptidase; amidase;
KW   carboxyesterase; amidase; glycosidase; MALDI; hydrolysis; detection;
KW   matrix-assisted laser desorption ionisation; fingerprinting; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "C nucleotide modified by hydroxyl group"
FT   modified_base   8
FT                   /*tag=  a
FT                   /note= "C nucleotide modified by hydroxyl group"
XX
PN   DE19714558-A1.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1997;   97DE-01014558.
XX
PR   09-APR-1997;   97DE-01014558.
XX
PA   (ENGE/) ENGELS J W.
XX
PI   Woerner K,  Faulstich K,  Brill H,  Engels JW;
XX
DR   WPI; 1998-543565/47.
XX
PT   Sequencing biopolymers - by mass spectrometric analysis of cleavage
PT   products.
XX
PS   Example 1; Page 3; 28pp; German.
XX
CC   AAV63047-V63052 are oligonucleotide primers used in a novel method for
CC   sequencing biopolymers with mass spectrometry. The method involves
CC   sequencing ribonucleic acids (RNA), nucleic acids (DNA), peptides or
CC   oligosaccharides by digestion of the RNA or DNA or peptide or
CC   oligosaccharide strands and comprises the strands being investigated
CC   being treated with specific exo-/endonucleases, -peptidases, -
CC   carboxyesterases, -amidases or -glycosidases or other sequence- or base-
CC   specifically cleaving compounds. The separation and detection of the
CC   fragments produced takes place following by mass spectrometry, primarily
CC   MALDI (matrix-assisted laser desorption ionisation), and various peak
CC   intensities, produced by enzymatic or chemical hydrolysis of the
CC   corresponding individual bonds, the mass spectra are enlisted for the
CC   interpretation of the sequence data. The method is useful for detecting
CC   or identifying organisms by DNA or RNA 'fingerprinting' or 'foot
CC   printing' or for determining the secondary structure of biopolymers
XX
SQ   Sequence 8 BP; 2 A; 2 C; 2 G; 0 T; 2 U; 0 Other;
```

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACATG 15
              ||||||||
Db          8 GTCACATG 1


RESULT 125
AAA81073
ID   AAA81073 standard; DNA; 8 BP.
XX
AC   AAA81073;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 386.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-00859954.
XX
PR   15-APR-1996;   96US-00632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT   other primer processes comprises primer walking of octamer
PT   oligonucleotides.
XX
PS   Example 8; Col 219-220; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and corresponding
CC   complementary sequences, where the library primer is complementary to a
CC   known sequence adjacent to the unknown sequence or is complementary to a
CC   sequence in a known extension product. The method is useful for DNA
CC   nucleotide sequencing, in PCR, and in other processes which make use of
CC   primers. The octamers are used to identify coding sequences. Primer
CC   walking using the octamer libraries is advantageous over other sequencing
CC   methods because it does not require multiple cloning steps nor subsequent
CC   template preparations, and it is a directed and methodical approach.
CC   AAA80688-A81253 represent the octamer primers used in the primer walking
CC   method of the invention
XX
SQ   Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 ATGGTCAC 12
              ||||||||
Db          1 ATGGTCAC 8


RESULT 126
AAV63049
ID   AAV63049 standard; DNA; 9 BP.
XX
AC   AAV63049;
XX
DT   15-JAN-1999  (first entry)
XX
DE   Synthetic DNA 9mer oligonucleotide primer.
XX
KW   Sequencing; biopolymer; mass spectrometry; nuclease; peptidase; amidase;
KW   carboxyesterase; amidase; glycosidase; MALDI; hydrolysis; detection;
KW   matrix-assisted laser desorption ionisation; fingerprinting; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "G nucleotide modified by hydroxyl group"
FT   modified_base   9
FT                   /*tag=  a
FT                   /note= "C nucleotide modified by hydroxyl group"
XX
PN   DE19714558-A1.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1997;   97DE-01014558.
XX
PR   09-APR-1997;   97DE-01014558.
XX
PA   (ENGE/) ENGELS J W.
XX
PI   Woerner K,  Faulstich K,  Brill H,  Engels JW;
XX
DR   WPI; 1998-543565/47.
XX
PT   Sequencing biopolymers - by mass spectrometric analysis of cleavage
PT   products.
XX
PS   Example 1; Page 3; 28pp; German.
XX
CC   AAV63047-V63052 are oligonucleotide primers used in a novel method for
CC   sequencing biopolymers with mass spectrometry. The method involves
CC   sequencing ribonucleic acids (RNA), nucleic acids (DNA), peptides or
CC   oligosaccharides by digestion of the RNA or DNA or peptide or
CC   oligosaccharide strands and comprises the strands being investigated
CC   being treated with specific exo-/endonucleases, -peptidases, -
CC   carboxyesterases, -amidases or -glycosidases or other sequence- or base-
CC   specifically cleaving compounds. The separation and detection of the
CC   fragments produced takes place following by mass spectrometry, primarily
CC   MALDI (matrix-assisted laser desorption ionisation), and various peak
CC   intensities, produced by enzymatic or chemical hydrolysis of the
CC   corresponding individual bonds, the mass spectra are enlisted for the
CC   interpretation of the sequence data. The method is useful for detecting
CC   or identifying organisms by DNA or RNA 'fingerprinting' or 'foot
CC   printing' or for determining the secondary structure of biopolymers
XX
SQ   Sequence 9 BP; 2 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACATG 15
              ||||||||
Db          1 GTCACATG 8


RESULT 127
AAV63048/c
ID   AAV63048 standard; RNA; 9 BP.
XX
AC   AAV63048;
XX
```

```
DT   15-JAN-1999  (first entry)
XX
DE   Synthetic RNA 9mer oligonucleotide primer.
XX
KW   Sequencing; biopolymer; mass spectrometry; nuclease; peptidase; amidase;
KW   carboxyesterase; amidase; glycosidase; MALDI; hydrolysis; detection;
KW   matrix-assisted laser desorption ionisation; fingerprinting; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /note= "C nucleotide modified by hydroxyl group"
FT   modified_base   9
FT                   /*tag= a
FT                   /note= "C nucleotide modified by hydroxyl group"
XX
PN   DE19714558-A1.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1997;   97DE-01014558.
XX
PR   09-APR-1997;   97DE-01014558.
XX
PA   (ENGE/) ENGELS J W.
XX
PI   Woerner K,  Faulstich K,  Brill H,  Engels JW;
XX
DR   WPI; 1998-543565/47.
XX
PT   Sequencing biopolymers - by mass spectrometric analysis of cleavage
PT   products.
XX
PS   Example 1; Page 3; 28pp; German.
XX
CC   AAV63047-V63052 are oligonucleotide primers used in a novel method for
CC   sequencing biopolymers with mass spectrometry. The method involves
CC   sequencing ribonucleic acids (RNA), nucleic acids (DNA), peptides or
CC   oligosaccharides by digestion of the RNA or DNA or peptide or
CC   oligosaccharide strands and comprises the strands being investigated
CC   being treated with specific exo-/endonucleases, -peptidases, -
CC   carboxyesterases, -amidases or -glycosidases or other sequence- or base-
CC   specifically cleaving compounds. The separation and detection of the
CC   fragments produced takes place following by mass spectrometry, primarily
CC   MALDI (matrix-assisted laser desorption ionisation), and various peak
CC   intensities, produced by enzymatic or chemical hydrolysis of the
CC   corresponding individual bonds, the mass spectra are enlisted for the
CC   interpretation of the sequence data. The method is useful for detecting
CC   or identifying organisms by DNA or RNA 'fingerprinting' or 'foot
CC   printing' or for determining the secondary structure of biopolymers
XX
SQ   Sequence 9 BP; 2 A; 2 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 5e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACATG 15
              ||||||||
Db          9 GTCACATG 2


RESULT 128
ADG13767
ID   ADG13767 standard; RNA; 9 BP.
XX
AC   ADG13767;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human HER1-4 Zinzyme target sequence #27.
XX
KW   Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
KW   HER4; hammerhead ribozyme; inozyme; zinzyme; DNAzyme; amberzyme; cancer;
KW   brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;
KW   prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW   stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW   head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW   multidrug resistant cancer.
XX
OS   Homo sapiens.
XX
PN   US2003186909-A1.
XX
PD   02-OCT-2003.
XX
PF   21-OCT-2002; 2002US-00277494.
XX
PR   27-JAN-1997;   97US-0036749P.
PR   04-DEC-1997;   97US-00985162.
PR   22-SEP-1999;   99US-00401063.
PR   03-MAY-2001; 2001US-00848754.
PR   25-JUL-2001; 2001US-00916466.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2004-032029/03.
XX
PT   New double stranded short interfering ribonucleic acid molecule for
PT   inhibiting expression of epidermal growth factor receptor gene.
XX
PS   Claim 7; SEQ ID NO 194; 113pp; English.
XX
CC   The invention relates to a double stranded short interfering RNA (siRNA)
CC   molecule that inhibits expression of epidermal growth factor receptor
CC   (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
CC   expression vector comprising a nucleic acid sequence encoding siRNA
CC   molecule(s) in a manner that allows expression of the nucleic acid
CC   molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
CC   amberzymes zinzymes and DNAzymes. The invention is used for inhibiting
CC   expression of EGFR. It can be used for treatment of cancer, prostate
CC   cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC   cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC   cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC   cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC   life in vitro , stability, and ease of introduction of oligonucleotide to
CC   target site. The present sequence is an EGFR/HER1-4 target sequence for
CC   an siRNA of the invention.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 2 G; 0 T; 2 U; 0 Other;

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity  75.0%;  Pred. No. 5e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CATGGTCA 11
              ||:||:||
Db          1 CAUGGUCA 8


RESULT 129
AAQ45113
ID   AAQ45113 standard; DNA; 10 BP.
XX
AC   AAQ45113;
XX
DT   25-MAR-2003  (revised)
DT   02-NOV-1994  (first entry)
XX
DE   5'-primer #24 for investigating gene expression.
XX
KW   PCR; polymerase chain reaction; amplification; primer; diagnosis;
```

```
KW   gene expression; cancer; ss.
XX
OS   Synthetic.
XX
PN   DE4317414-C1.
XX
PD   21-APR-1994.
XX
PF   18-MAY-1993;   93DE-04317414.
XX
PR   18-MAY-1993;   93DE-04317414.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Strauss M,  Bauer D;
XX
DR   WPI; 1994-110647/14.
XX
PT   Diagnostic agent for investigating gene expression - comprises
PT   oligonucleotide primer pairs formed from labelled 5'- and 3'-
PT   oligonucleotide primers.
XX
PS   Claim 7; Col 7; 6pp; German.
XX
CC   AAQ45090-Q45115 are preferred 5'-primers for use with a pool of at least
CC   12 3'-primers coupled with a detectable label. The 5'-primers all contain
CC   equal numbers of G+C and A+T nucleotides. The 288 (or more) combinations
CC   of 5'- and 3'-primers are used in PCR amplifications as part of a method
CC   for diagnosing gene expression. The amplified fragments are separated by
CC   non-denaturing PAGE and the band pattern is compared to a standard.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 130
AAQ96922
ID   AAQ96922 standard; DNA; 10 BP.
XX
AC   AAQ96922;
XX
DT   16-OCT-2003  (revised)
DT   26-MAR-1996  (first entry)
XX
DE   HIV-1 NL4-3 nef gene nucleotide deletion 517.
XX
KW   HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9521912-A1.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-AU000063.
XX
PR   14-FEB-1994;   94AU-00003864.
PR   21-FEB-1994;   94AU-00004002.
PR   23-DEC-1994;   94AU-00000284.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA   (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI   Deacon NJ,  Learmont JC,  Mcphee DA,  Crowe S,  Cooper D;
XX
DR   WPI; 1995-293115/38.
XX
PT   New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT   LTR region - can be used in a vaccine to inhibit/reduce productive
PT   infection in an individual by a pathogenic strain.
XX
PS   Claim 13; Page 195; 301pp; English.
XX
CC   Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC   more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC   decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC   AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC   resulting avirulent HIV strains are still capable of inducing an immune
CC   response in humans, and enable the generation of therapeutic, diagnostic
CC   and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           1 ATGGATGA 8


RESULT 131
AAQ96920
ID   AAQ96920 standard; DNA; 10 BP.
XX
AC   AAQ96920;
XX
DT   16-OCT-2003  (revised)
DT   26-MAR-1996  (first entry)
XX
DE   HIV-1 NL4-3 nef gene nucleotide deletion 515.
XX
KW   HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9521912-A1.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-AU000063.
XX
PR   14-FEB-1994;   94AU-00003864.
PR   21-FEB-1994;   94AU-00004002.
PR   23-DEC-1994;   94AU-00000284.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA   (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI   Deacon NJ,  Learmont JC,  Mcphee DA,  Crowe S,  Cooper D;
XX
DR   WPI; 1995-293115/38.
XX
PT   New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT   LTR region - can be used in a vaccine to inhibit/reduce productive
PT   infection in an individual by a pathogenic strain.
XX
PS   Claim 13; Page 194; 301pp; English.
XX
CC   Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC   more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC   decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC   AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC   resulting avirulent HIV strains are still capable of inducing an immune
CC   response in humans, and enable the generation of therapeutic, diagnostic
CC   and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
```

```
CC   standardise OS field)
XX
SQ   Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          3 ATGGATGA 10


RESULT 132
AAQ96921
ID   AAQ96921 standard; DNA; 10 BP.
XX
AC   AAQ96921;
XX
DT   16-OCT-2003  (revised)
DT   26-MAR-1996  (first entry)
XX
DE   HIV-1 NL4-3 nef gene nucleotide deletion 516.
XX
KW   HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9521912-A1.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-AU000063.
XX
PR   14-FEB-1994;   94AU-00003864.
PR   21-FEB-1994;   94AU-00004002.
PR   23-DEC-1994;   94AU-00000284.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA   (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI   Deacon NJ,  Learmont JC,  Mcphee DA,  Crowe S,  Cooper D;
XX
DR   WPI; 1995-293115/38.
XX
PT   New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT   LTR region - can be used in a vaccine to inhibit/reduce productive
PT   infection in an individual by a pathogenic strain.
XX
PS   Claim 13; Page 194; 301pp; English.
XX
CC   Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC   more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC   decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC   AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC   resulting avirulent HIV strains are still capable of inducing an immune
CC   response in humans, and enable the generation of therapeutic, diagnostic
CC   and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 133
AAT35724
ID   AAT35724 standard; DNA; 10 BP.
XX
AC   AAT35724;
XX
DT   08-OCT-1996  (first entry)
XX
DE   Primer UBC556 for V.dahliae RAPD reaction.
XX
KW   RAPD; random amplified polymorphic DNA; diagnostic assay; quantitative;
KW   PCR; primer; qualitative; soil sample; agricultural field; potatoe;
KW   V.albo-atrum; soil fumigation; amplify; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   US5527671-A.
XX
PD   18-JUN-1996.
XX
PF   07-NOV-1994;   94US-00335565.
XX
PR   07-NOV-1994;   94US-00335565.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   German TL,  Li K,  Rouse DI;
XX
DR   WPI; 1996-299849/30.
XX
PT   Assay for Verticillium dahliae - by amplification of specific DNA
PT   sequence.
XX
PS   Example; Col 9; 16pp; English.
XX
CC   AAT35710-T35738 represent amplification primers used in a random
CC   amplified polymorphic DNA (RAPD) reaction on V.dahliae DNA. These
CC   sequences were used to isolate the sequence represented by AAT35706 for
CC   use in the diagnostic assays of the invention. The qualitative assays of
CC   the invention comprise analysing a sample for the presence of the
CC   V.dahliae sequence. Detection of the V.dahliae sequence in the sample
CC   shows that the sample is infected by V.dahliae. A quantitative assay of
CC   the invention, comprises taking a sample and isolating nucleic acids from
CC   it. A sequence that acts as an internal standard (see AAT35707) is added
CC   to the isolated nucleic acids. The internal standard competes with the
CC   V.dahliae sequence for the PCR primers used in the reaction (such as the
CC   sequences represented by AAT35708 and AAT35709). The amplified portion of
CC   the internal standard is a different size to the amplified portion of the
CC   V.dahliae sequence. The amounts of amplified DNA of each sequence is then
CC   compared to indicate the number of V.dahliae present in the sample. The
CC   sample used in these assays is normally a soil sample from an
CC   agricultural field that is going to be used for growing potatoes. These
CC   assays are faster and more accurate than methods based on culturing soil
CC   samples in selective media. The assays can also distinguish between
CC   V.dahliae and V.albo-atrum. By using these assays, unnecessary soil
CC   fumigation can be avoided
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          1 ATGGATGA 8


RESULT 134
AAT98841/c
ID   AAT98841 standard; DNA; 10 BP.
XX
AC   AAT98841;
XX
DT   20-MAR-1998  (first entry)
```

XX
DE Binding site BSN5-1 identified using the method of the invention.
XX
KW Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
XX
PD 31-JUL-1997.
XX
PF 24-JAN-1997; 97WO-US001230.
XX
PR 24-JAN-1996; 96US-00590571.
XX
PA (UYYA) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
DR WPI; 1997-393714/36.
XX
PT Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
               ||||||||
Db         10 CATGGATG 3
```

RESULT 135
AAV68349/c
ID AAV68349 standard; DNA; 10 BP.
XX
AC AAV68349;
XX
DT 10-MAR-1999 (first entry)
XX
DE Adapter primer oligonucleotide 2 for CAG repeat analysis.
XX
KW CAG repeat; human; genome analysis; adapter primer; medical diagnostic;
KW nucleic acid analysis; variation assessment; neurological disease;
KW Huntington's chorea; PCR suppression; ss.
XX
OS Synthetic.
XX
PN WO9849345-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US008616.
XX
PR 29-APR-1997; 97US-0045078P.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Smith CL;
XX
DR WPI; 1998-594983/50.
XX
PT Analysing nucleic acid samples - using amplification primers which
PT contain CAG or CTG tri:nucleotide repeats for differential display of
PT samples from different sources.
XX
PS Example; Page 18; 44pp; English.
XX
CC This sequence represents an adapter primer oligonucleotide. It was used
CC to isolate CAG repeat containing sequences from the human genome to test
CC the method of the invention. The method is for analysing nucleic acids in
CC a sample, and comprises: (a) providing a sample containing nucleic acid,
CC a first oligonucleotide primer comprising a CTG repeat, a second
CC oligonucleotide primer comprising a CAG repeat and a polymerase and PCR
CC reagents; (b) preparing said nucleic acid so that it is amplifiable; (c)
CC amplifying the nucleic acid with the first and second primers; and (d)
CC detecting the amplified product. The method is used to distinguish
CC between the expression of genes in two or more biological samples, e.g.
CC body fluids, cells, solid tissue or solid and liquid foods. It can be
CC used in medical diagnostics, e.g. to differentiate between normal and
CC diseased tissue or to assess the variation within monozygotic twin pairs.
CC The method allows the isolation and analysis of genome subsets containing
CC CAG repeats which are known to be important in a number of neurological
CC diseases including Huntington's chorea. The method uses PCR suppression,
CC in which only fragments which contain a target repeat are efficiently
CC amplified. This allows accurate identification of differentially
CC expressed genes in various cell types. Genome complexity is reduced by
CC the new method which targets genomic subsets containing CAG repeats
XX
SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 ACATGGAT 18
               ||||||||
Db          9 ACATGGAT 2
```

RESULT 136
AAT99553
ID AAT99553 standard; DNA; 10 BP.
XX
AC AAT99553;
XX
DT 08-JUN-1998 (first entry)
XX
DE Random 10-mer primer used in epoxide hydrolase mEH gene RT-PCR.
XX
KW Cell growth regulatory gene; mEH; microsomal epoxide hydrolase; rat;
KW tumour; cancer; diagnosis; gene therapy; RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9745542-A2.
XX
PD 04-DEC-1997.
XX
PF 29-MAY-1997; 97WO-US009584.
XX

```
PR   29-MAY-1996;   96US-0018557P.
XX
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Beaudry GA,  Bertelsen AH,  Galella E,  Madden SI;
XX
DR   WPI; 1998-032649/03.
XX
PT   DNA encoding mammalian growth response protein CGR11 or CGR19 - useful to
PT   suppress or diagnose cancer, also similar use of SM20 or mEH protein.
XX
PS   Example 2; Page 16; 46pp; English.
XX
CC   This random 10-mer primer was used with an oligo-dT primer (see AAT99552)
CC   in an RT-PCR amplification of rat embryo fibroblast REF-112 cell RNA.
CC   This was performed in order to identifying p53 regulated genes. One
CC   transcript that was upregulated specifically in cells harboring wild-type
CC   p53 protein was characterised. A previously known gene, mEH (microsomal
CC   epoxide hydrolase), was identified. 2 Novel cell growth regulatory genes,
CC   CGR11 (see AAV04008) and CGR19 (see AAV04010), were also isolated. These
CC   genes and the novel CGR11 and CGR19 growth regulatory proteins (see
CC   AAW38423 and AAW38425) can be used in methods for the diagnosis and
CC   treatment of cancer
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 137
AAX02707
ID   AAX02707 standard; DNA; 10 BP.
XX
AC   AAX02707;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Barley HPPD primer #13.
XX
KW   HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
KW   transgenic; plant cell; callus tissue, protoplast; electroporation;
KW   particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
KW   sunflower; tobacco; ss.
XX
OS   Hordeum vulgare.
XX
PN   DE19730066-A1.
XX
PD   21-JAN-1999.
XX
PF   14-JUL-1997;   97DE-01030066.
XX
PR   14-JUL-1997;   97DE-01030066.
XX
PA   (BADI ) BASF AG.
XX
PI   Seulberger H,  Lerchl J,  Schmidt R,  Kurpinska K,  Falk J;
XX
DR   WPI; 1999-096742/09.
XX
PT   DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing
PT   plants with increased vitamin E content, etc.
XX
PS   Example 1; Page 9; 26pp; German.
XX
CC   AAX02695-X02708 are primers used in the isolation of a novel barley
CC   (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
CC   protein is useful for plant transformation to produce transgenic plants
CC   especially where an expression cassette is introduced into a plant cell,
CC   callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
CC   transformation, electroporation or particle bombardment and where the
CC   plants are selected from soya, barley, wheat, oilseed rape, maize and
CC   sunflower, or where the DNA is expressed in tobacco plants, especially in
CC   leaves or seeds
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 138
AAX18375
ID   AAX18375 standard; DNA; 10 BP.
XX
AC   AAX18375;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 16.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10
```

```
RESULT 139
AAX15555
ID   AAX15555 standard; DNA; 10 BP.
XX
AC   AAX15555;
XX
DT   06-MAY-1999  (first entry)
XX
DE   Differential display RT-PCR primer used in analysis of murine TG.
XX
KW   Origin binding protein Binding site III sequence; HSV-1; HSV-2;
KW   viral infection; viral reactivation; interferon regulatory factor-1;
KW   IRF-1; TIS7; interferon-alpha; IFN-alpha; IFN-beta; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9901464-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013733.
XX
PR   03-JUL-1997;   97US-0051633P.
PR   01-AUG-1997;   97US-0054515P.
PR   01-APR-1998;   98US-0080352P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (WIST-) WISTAR INST.
XX
PI   Berger SL,  Fraser NW,  Leary JJ,  Tal-Singer R;
XX
DR   WPI; 1999-105992/09.
XX
PT   Treating viral infection or reactivation, particularly Herpesvirus -
PT   using compounds which modulate interferon pathways.
XX
PS   Example 3; Page 39; 40pp; English.
XX
CC   Differential display RT-PCR primers AAX15549-70 were used in the analysis
CC   of murine trigeminal ganglia (TG) explants, to determine the level of
CC   viral reactivation after treatment with the composition of the invention.
CC   The specification describes a for treating viral infection or
CC   reactivation. The method comprises contacting an individual with a
CC   compound which is an antagonist of the reaction between the origin
CC   binding protein Binding site III sequence from Herpes simplex virus (HSV)
CC   -1 and HSV-2 and interferon regulatory factor-1 (IRF-1). Alternatively,
CC   the compound lowers the level of IRF-1, TIS7, interferon (IFN)-alpha, or
CC   IFN-beta. The method can be used to treat viral reactivation in HSV
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 140
AAZ77696
ID   AAZ77696 standard; DNA; 10 BP.
XX
AC   AAZ77696;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:124.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 67; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
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CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           2 ATGGATGA 9


RESULT 141
AAZ79089
ID   AAZ79089 standard; DNA; 10 BP.
XX
AC   AAZ79089;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1517.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 108; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           7 GGTCACAT 14
               ||||||||
Db           1 GGTCACAT 8


RESULT 142
AAZ84009
ID   AAZ84009 standard; DNA; 10 BP.
XX
AC   AAZ84009;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3243.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
```

```
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 145; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 143
AAZ34693
ID   AAZ34693 standard; DNA; 10 BP.
XX
AC   AAZ34693;
XX
DT   15-FEB-2000  (first entry)
XX
DE   D24 randomer used in DDRT-PCR identification of ERAB.
XX
KW   Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;
KW   Leydig cell; differential display RT-PCR; DDRT-PCR;
KW   short chain alcohol dehydrogenase; SCAD; testis; marker; spermatogenesis;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO9954347-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-EP002610.
XX
PR   17-APR-1998;   98US-0082257P.
XX
PA   (HORM-) INST HORMON & FORTPFLANZUNGSFORSCHUNG GM.
XX
PI   Ivell R,  Spiess A,  Balvers M,  Jaehner D,  Hansis C;
XX
DR   WPI; 2000-052699/04.
XX
PT   Novel differential display reverse transcription PCR method used to
PT   detect genes expressed in mutant tissues.
XX
PS   Disclosure; Page 26; 40pp; English.
XX
CC   This sequence represents decamer D24, which was used in a novel
CC   differential display RT-PCR (DDRT-PCR) method of detecting genes
CC   expressed in tissues, especially mutant tissue. RNA isolated from adult
CC   male w/wv azoospermic mutant mice testis was subjected to reverse
CC   transcription. 324 PCRs were performed on the resulting cDNA using 3'
CC   clamp primers (see Z3467-69) and variable decamer 5' primers D1-D26 (see
CC   AAZ34670-95). Differentially expressed clones were used as probes in
CC   northern hybridisation, and a novel gene product that was preferentially
CC   upregulated in w/wv mouse testis was identified and termed Alzheimer-
CC   associated beta-amyloid binding protein (ERAB, see AAZ32239)
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 144
AAA61006/c
ID   AAA61006 standard; DNA; 10 BP.
XX
AC   AAA61006;
XX
DT   11-OCT-2000  (first entry)
XX
DE   Protein binding sequence BSN5-1.
XX
KW   Protein binding sequence; DNA binding factor; protein inactivation;
KW   protein selection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   protein_bind    1. .10
FT                   /*tag=  a
FT                   /bound_moiety= "Pit-1"
XX
PN   US6066452-A.
XX
PD   23-MAY-2000.
XX
```

```
PF   06-AUG-1997;   97US-00906691.
XX
PR   24-JAN-1996;   96US-00590571.
PR   24-JAN-1997;   97WO-US001230.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kulkarni P,  Nallur GN,  Weissman SM;
XX
DR   WPI; 2000-421703/36.
XX
PT   Identifying and isolating binding proteins, and nucleotide recognition
PT   sequences for DNA-binding proteins by mixing oligonucleotide sequences
PT   comprising randomized internal sequences with a DNA-binding protein
PT   source.
XX
PS   Example 3; Col 13; 26pp; English.
XX
CC   The present sequence is a randomly generated binding site sequence, which
CC   has been shown to be similar to the sequence which binds to the Pit-1
CC   transcription factor. This was used to demonstrate the invention, which
CC   comprises a method for simultaneously selecting those sequences which
CC   bind to different DNA-binding proteins. These sequences can then be
CC   analysed and used to identify other DNA-binding proteins, as well as
CC   being used to inactivate or specifically select particular proteins
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CATGGATG 19
               ||||||||
Db          10 CATGGATG 3


RESULT 145
AAH18801/c
ID   AAH18801 standard; DNA; 10 BP.
XX
AC   AAH18801;
XX
DT   25-JUN-2001  (first entry)
XX
DE   Human IL4 allele-specific primer-extension oligo SEQ ID NO: 60.
XX
KW   Human; interleukin-4; IL4; single nucleotide polymorphism; SNP; atopy;
KW   inflammatory disorder; immune disorder; population diversity;
KW   paternity test; forensic test; cytokine; chromosome 5q31.1; probe;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200123404-A1.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US026608.
XX
PR   30-SEP-1999;   99US-0156825P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Denton RR,  Nandabalan K,  Stephens JC;
XX
DR   WPI; 2001-316132/33.
XX
PT   Polynucleotide comprising novel single nucleotide polymorphisms in human
PT   interleukin-4 gene for use in studying expression, function of
PT   interleukin-4, in developing drugs, diagnosis and treatment of immune
PT   disorders.
XX
PS   Disclosure; Page 17; 71pp; English.
XX
CC   The present invention provides the protein, cDNA and gene of human
CC   interleukin-4 (IL4). The coding sequences for this protein contain single
CC   nucleotide polymorphisms (SNPs) which may be associated with differences
CC   in susceptibility to atopy, inflammatory and immune diseases and
CC   different drug responses. They may also be used in applications such as
CC   forensic and paternity testing and studying population diversity and
CC   anthropological lineage. The IL4 gene is found on human chromosome 5q31.1
XX
SQ   Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 CTCATGGT 9
                ||||||||
Db           8 CTCATGGT 1


RESULT 146
AAF43831/c
ID   AAF43831 standard; DNA; 10 BP.
XX
AC   AAF43831;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11970.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 377; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
```

CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGGTCACA 13
||||||||
Db 9 TGGTCACA 2

RESULT 147
AAF43028/c
ID AAF43028 standard; DNA; 10 BP.
XX
AC AAF43028;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11167.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 348; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGGTCACA 13
||||||||
Db 10 TGGTCACA 3

RESULT 148
ABL88465
ID ABL88465 standard; DNA; 10 BP.
XX
AC ABL88465;
XX
DT 16-MAY-2002 (first entry)
XX
DE Pain regulated gene related PCR primer Deka24.
XX
KW Pain; analgesic; gene therapy; neurological disorder;
KW neurodegenerative disease; primer; ss.
XX
OS Synthetic.
XX
PN WO200212338-A2.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001WO-EP009011.
XX
PR 03-AUG-2000; 2000DE-01037759.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Gillen C, Wetzels I, Wnendt S, Weihe E, Schaefer MK;
XX
DR WPI; 2002-257469/30.
XX
PT Identifying pain-regulating compounds, useful for treating chronic pain
PT and for diagnosis, by measuring binding of compounds to specific peptides
PT and proteins.
XX
PS Example 1; Page 62; 213pp; German.
XX
CC The invention relates to identifying pain-regulating substances (A)
CC comprises (i) incubating a test substance with a cell (or preparation
CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-
CC ABB85037) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain,
CC including use in gene therapy. The same materials can also be used for

```
CC   diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC   present sequence is that of a PCR primer, used in examples of the
CC   invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 149
ABL42924
ID   ABL42924 standard; cDNA; 10 BP.
XX
AC   ABL42924;
XX
DT   12-APR-2002  (first entry)
XX
DE   Human maturation/activation dendritic cell expression gene tag #298.
XX
KW   Human; maturation/activation dendritic cell expression gene; tag;
KW   maturation; activation; dendritic cell; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001327293-A.
XX
PD   27-NOV-2001.
XX
PF   22-MAY-2000; 2000JP-00150562.
XX
PR   22-MAY-2000; 2000JP-00150562.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-127070/17.
XX
PT   Human maturation/activation dendritic cell expression gene group.
XX
PS   Claim 19; Page 17; 41pp; Japanese.
XX
CC   The present invention describes a human maturation/activation dendritic
CC   cell (DC) expression gene group consisting of 100 genes which show the
CC   highest expression among the genes expressed in human maturation/
CC   activation DC. Also described are: (1) a protein expressed by the above
CC   human maturation/activation DC expression gene; (2) an antibody against
CC   the protein; and (3) an antagonist against the expression of each gene
CC   belonging to the above gene group. The gene group is useful for the
CC   treatment and the diagnosis of various human diseases related to human
CC   DC. ABL42627 to ABL42926 represent specifically claimed human
CC   maturation/activation DC expression gene tags from the present invention
XX
SQ   Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 150
ABK92583/c
ID   ABK92583 standard; DNA; 10 BP.
XX
AC   ABK92583;
XX
DT   20-AUG-2002. (first entry)
XX
DE   Primer-extension oligonucleotide #8 to detect human CHRM4 polymorphisms.
XX
KW   Human; single nucleotide polymorphism; SNP; CHRM4; haplotyping;
KW   chromosome 11p12-p11.2; cholinergic receptor muscarinic 4; genotyping;
KW   Alzheimer's disease; neurological disorder; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200236609-A2.
XX
PD   10-MAY-2002.
XX
PF   31-OCT-2001; 2001WO-US045709.
XX
PR   31-OCT-2000; 2000US-0244627P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (PETE/) PETERSON N.
PA   (ROUN/) ROUNDS E.
XX
PI   Denton RR,  Duda A,  Gilson CR,  Kazemi A,  Nandabalan K,  Tirrell C;
XX
DR   WPI; 2002-489997/52.
XX
PT   Novel genetic variants of cholinergic receptor muscarinic 4 useful in
PT   studying expression and function of protein, and for screening drugs to
PT   treat diseases e.g. Alzheimer's disease and other neurological disorders.
XX
PS   Claim 16; Page 14; 63pp; English.
XX
CC   The present invention relates to novel single nucleotide polymorphisms
CC   (SNPs) in the human cholinergic receptor, muscarinic 4 (CHRM4) gene
CC   located on chromosome 11p12-p11.2, and methods for haplotyping and/or
CC   genotyping the CHRM4 gene. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC   primer-extension oligonucleotides for detecting the CHRM4 gene
CC   polymorphisms. The polynucleotides and screened compounds are useful for
CC   the treatment of diseases associated with CHRM4 activity, such as
CC   Alzheimer's disease and other neurological disorders. ABK92576-ABK92587
CC   represent primer-extension oligonucleotides for detecting human CHRM4
CC   gene polymorphisms
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          9 TCATGGTC 2


RESULT 151
AAD45283
ID   AAD45283 standard; DNA; 10 BP.
XX
AC   AAD45283;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PON-1 gene polymorphism detecting primer #15.
XX
KW   Human; paraoxonase 1; PON1; single nucleotide polymorphism; transgenic;
KW   SNP; drug screening; organo-phosphorous metabolism; target validation;
KW   atherosclerosis; type II diabetes; gene therapy; antilipaemic; primer;
KW   ss.
XX
OS   Homo sapiens.
XX
```

PN WO200266680-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001WO-US046896.
XX
PR 16-FEB-2001; 2001WO-US005126.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Chew A, Choi JY, Denton RR, Nandabalan K, Parks KE;
PI Stephens JC;
XX
DR WPI; 2002-682769/73.
XX
PT New genetic variants of human paraoxonase 1 (PON1) gene with
PT polymorphisms, useful for treating disorders associated with PON1 isogene
PT activity e.g. atherosclerosis or diabetes, or for screening drugs for
PT treating these diseases.
XX
PS Claim 17; Page 15; 118pp; English.
XX
CC The invention relates to methods for haplotyping human paraoxonase 1
CC (PON1) gene. It also relates to the single nucleotide polymorphisms (SNP)
CC in PON-1 gene. Polymorphic variants of the PON1 gene are useful in
CC studying the expression and function of PON1, and in expressing PON1
CC proteins for use in screening candidate drugs to treat diseases
CC associated with PON1 activity, e.g. disorders of lipid and organo-
CC phosphorous metabolism such as atherosclerosis or type II diabetes. They
CC are also used in gene therapy. Establishing PON1 haplotype or haplotype
CC pair of an individual is useful for improving the efficiency and
CC reliability of several steps including target validation, in the
CC discovery and development of drugs for treating diseases associated with
CC PON1 activity. Transgenic animals are useful for studying expression of
CC the PON1 isogenes in vivo. The present sequence is a primer used to
CC detect human PON-1 gene polymorphisms
XX
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCTCATGG 8
              ||||||||
Db          3 CCTCATGG 10
```

RESULT 152
ABK72438/c
ID ABK72438 standard; DNA; 10 BP.
XX
AC ABK72438;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human HTR5A gene allele-specific oligonucleotide PCR primer #40.
XX
KW Human; 5-hydroxytryptamine receptor 5A; HTR5A; serotonin; primer; ss;
KW neuroprotective; neurological disease; depression; epilepsy; PCR;
KW gene therapy; single nucleotide polymorphism; haplotype pair;
KW chromosome 7q36.1.
XX
OS Homo sapiens.
XX
PN WO200222887-A1.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US029210.
XX
PR 15-SEP-2000; 2000US-0233051P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Koshy B, Sanchis A, Tirrell C;
XX
DR WPI; 2002-393978/42.
XX
PT Novel genetic variants of 5-Hydroxytryptamine (Serotonin) Receptor 5A
PT isogenes, useful for improving efficiency and reliability in drug
PT development for treating neurological diseases.
XX
PS Claim 19; Page 15; 134pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding human 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A). A
CC method for haplotyping the HTR5A gene in an individual comprises
CC identifying the nucleotide at one or more polymorphic sites and
CC determining whether one of the copies of the gene is defined by one of
CC the HTR5A haplotypes given in the specification or whether both copies
CC are defined by a haplotype pair. This method is useful in genotyping,
CC whereby all possible haplotype pairs can be assigned to specific
CC genotypes. An association between a trait and a haplotype or haplotype
CC pair of the HTR5A gene can be identified by comparing the frequency of
CC the haplotype or haplotype pair in a population exhibiting the trait with
CC the frequency of the haplotype or haplotype pair in a reference
CC population, where a higher haplotype frequency in the trait population
CC indicates the trait is associated with the haplotype or haplotype pair.
CC HTR5A and its corresponding DNA are used for studying the expression and
CC function of HTR5A, and in screening for candidate drugs to treat diseases
CC related to HTR5A activity, such as neurological disorders, including
CC depression and epilepsy. Sequences ABK72399-ABK72438 represent allele-
CC specific oligonucleotide PCR primers used for detecting HTR5A gene
CC polymorphisms
XX
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCTCATGG 8
              ||||||||
Db          8 CCTCATGG 1
```

RESULT 153
AAL46123/c
ID AAL46123 standard; DNA; 10 BP.
XX
AC AAL46123;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human pro-platelet basic protein DNA primer extension oligo #12.
XX
KW Human; pro-platelet basic protein; PPBP; metabolic disorder;
KW immunological disorder; SNP; single nucleotide polymorphism; ss;
KW immunomodulator; chromosome 4q12-13; primer extension oligonucleotide.
XX
OS Homo sapiens.
XX
PN WO200229114-A1.
XX
PD 11-APR-2002.
XX
PF 09-OCT-2001; 2001WO-US031509.
XX
PR 06-OCT-2000; 2000US-0238692P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Russo DP;
XX
DR WPI; 2002-394352/42.

```
XX
PT   New Pro-Platelet Basic Protein (PPBP) gene polymorphic variants, useful
PT   for studying the expression and function of PPBP and screening candidate
PT   drugs for treating disorders associated with PPBP activity, e.g.
PT   immunological disorders.
XX
PS   Claim 15; Page 13; 68pp; English.
XX
CC   The present invention provides the protein, cDNA and genomic sequences of
CC   human pro-platelet basic protein (PPBP) and single nucleotide
CC   polymorphisms (SNPs) identified therein. The polymorphic variants are
CC   useful in studying the expression and function of PPBP, in expressing
CC   PPBP protein for use in screening for candidate drugs to treat diseases
CC   related to PPBP activity, in studying the effect of the variation on the
CC   biological activity of PPBP, and the binding affinity of candidate drugs
CC   targeting PPBP for the treatment of disorders associated with PPBP
CC   activity, e.g. metabolic and immunological disorders. The present
CC   sequence is an allele specific primer extension oligonucleotide for the
CC   gene of the invention
XX
SQ   Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACAT 14
              ||||||||
Db          9 GGTCACAT 2


RESULT 154
ABI99138/c
ID   ABI99138 standard; DNA; 10 BP.
XX
AC   ABI99138;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Human PCDH2 ASO PCR primer SEQ ID NO 95.
XX
KW   Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
KW   single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
KW   allele-specific oligonucleotide; ASO; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200194361-A2.
XX
PD   13-DEC-2001.
XX
PF   06-JUN-2001; 2001WO-US018321.
XX
PR   06-JUN-2000; 2000US-0209564P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kliem SE,  Koshy B,  Tanguay DA;
XX
DR   WPI; 2002-097928/13.
XX
PT   New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
PT   useful in expressing PCDH2 protein for screening candidate drugs to treat
PT   diseases related to PCDH2 activity.
XX
PS   Claim 18; Page 14; 127pp; English.
XX
CC   The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
CC   comprising determining which of the haplotypes given in the specification
CC   defines one or both copies of the individual's pCDH2 gene. The
CC   polymorphisms are within a 30244 base pair sequence (ABA05413), fully
CC   defined in the specification. The polymorphic variants are useful in
CC   studying the expression and function of PCDH2, in expressing PCDH2
CC   protein for use in screening for candidate drugs to treat diseases such
CC   as cancer, related to PCDH2 activity, in studying the effect of the
CC   variation on the biological activity of PCDH2 and the binding affinity of
CC   candidate drugs targeting PCDH2. The haplotyping methods are useful in
CC   validating PCDH2 as a candidate target for treating a specific condition
CC   or disease predicted to be associated with PCDH2 activity or in the
CC   design of clinical trials of candidate drugs for treating a specific
CC   condition or disease associated with PCDH2 activity. The present sequence
CC   is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
CC   the invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGGTCACA 13
              ||||||||
Db          9 TGGTCACA 2


RESULT 155
AAL39800/c
ID   AAL39800 standard; DNA; 10 BP.
XX
AC   AAL39800;
XX
DT   05-SEP-2002  (first entry)
XX
DE   SMOH polymorphism detecting primer SEQ ID No 115.
XX
KW   Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;
KW   human smoothened Drosophila homologue; basal cell carcinoma; BCC;
KW   gene therapy; antisense gene therapy; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200229004-A2.
XX
PD   11-APR-2002.
XX
PF   04-OCT-2001; 2001WO-US031304.
XX
PR   04-OCT-2000; 2000US-0237871P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Choi JY,  Koshy B,  Lee HH,  Sausker EA;
XX
DR   WPI; 2002-519113/55.
XX
PT   New genetic variants of smoothened Drosophila homolog (SMOH) gene useful
PT   for therapeutic purposes and for expressing SMOH protein useful in
PT   identifying drugs to treat basal cell carcinomas.
XX
PS   Claim 17; Page 15; 179pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising a sequence
CC   which is a polymorphic variant of a reference sequence for the human
CC   smoothened Drosophila homologue (SMOH) gene or its fragment, or a
CC   polymorphic variant of a reference sequence for a SMOH cDNA or its
CC   fragment. A new isolated polypeptide is useful for screening for drugs
CC   targeting the polypeptide. A new method is useful for identifying an
CC   association between a trait such as a clinical response to a drug
CC   targeting SMOH and a haplotype or haplotype pair of SMOH gene. The
CC   methods have applicability in developing diagnostic tests and therapeutic
CC   treatments for basal cell carcinomas (BCCs). The isolated polynucleotide
CC   is useful for studying the expression and function of SMOH and expressing
CC   SMOH protein for use in screening for candidate drugs to treat diseases
CC   related to SMOH activity. The polymorphism and haplotype data are useful
CC   for validating whether SMOH is a suitable target for drugs to treat BCCs,
CC   screening for the drugs and reducing bias in clinical trials of the
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CC   drugs. The isolated polynucleotide is useful for therapeutic purposes.
CC   The new method, an oligonucleotide and kit of the invention are useful
CC   for determining whether an individual has one of the haplotypes or the
CC   haplotype pairs. The polynucleotides of the invention can be used to
CC   treat disorders by gene therapy and antisense gene therapy. This
CC   polynucleotide sequence represents a primer used for detecting human
CC   smoothened Drosophila homologue gene polymorphisms of the invention
XX
SQ   Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
               ||||||||
Db          8 CATGGATG 1


RESULT 156
ADD07256
ID   ADD07256 standard; DNA; 10 BP.
XX
AC   ADD07256;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Mouse differential display RT-PCR primer #7.
XX
KW   PCR; ss; interferon regulatory factor; IRF-1; IRF-2; herpes; antiviral;
KW   transcription factor; virucide; vaccine; interferon; mouse; primer;
KW   differential display; RT-PCR; reverse transcriptase PCR.
XX
OS   Mus musculus.
XX
PN   US2003104356-A1.
XX
PD   05-JUN-2003.
XX
PF   26-MAR-2002; 2002US-00108164.
XX
PR   22-NOV-1999;   99US-00424348.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Berger SL;
XX
DR   WPI; 2003-801223/75.
XX
PT   Treating infection or reactivation caused by Herpes virus comprises using
PT   antagonist of Herpes Simplex virus polynucleotide sequence and interferon
PT   regulatory factor-1.
XX
PS   Example 3; SEQ ID NO 104; 53pp; English.
XX
CC   The invention relates to treating viral infection or reactivation
CC   comprising contacting an individual with an antagonist of the interaction
CC   between a Herpes Simplex virus (HSV) polynucleotide sequence appearing as
CC   ADD07153 and interferon regulatory factor-1 (IRF-1, a transcription
CC   factor of the interferon regulatory pathway). Also included are an
CC   isolated HSV polynucleotide comprising ADD07153, a composition comprising
CC   a HSV polypeptide involved in viral infection or reactivation, screening
CC   for compounds capable of inhibiting specific binding of IRF-1 to a
CC   polynucleotide, screening for compounds capable of inhibiting specific
CC   binding of IRF-1 to IRF-1:IRF-BP (undefined) complex, a compound capable
CC   of agonising or antagonising any compound in IRF-1 and/or interferon
CC   genetic regulatory pathway and a composition for comprising an HSV IRF-1
CC   binding site consensus sequence. The method is useful for treating
CC   infection or reactivation caused by Herpes virus, e.g., HSV-1 or HSV-2
CC   infections and for cytomegalovirus, Epstein Barr virus and zoster virus
CC   infection. The HSV polypeptide and polynucleotides may also be useful as
CC   antiviral vaccines. An experiment was performed where cDNA from the
CC   transgeminal ganglia of mice infected with HSV was isolated by
CC   differential display reverse transcriptase PCR (DDRT-PCR). The present
CC   sequence is a DDRT-PCR primer used in the experiment.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 157
ADE13925
ID   ADE13925 standard; DNA; 10 BP.
XX
AC   ADE13925;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Optineurin promoter motif, repeat element or regulatory region #34.
XX
KW   Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW   SNP; glaucoma; progressive ocular hypertensive disorder;
KW   glaucoma related disorder; motif; repeat element; regulatory region.
XX
OS   Homo sapiens.
XX
PN   US2003190617-A1.
XX
PD   09-OCT-2003.
XX
PF   06-MAR-2002; 2002US-00091281.
XX
PR   06-MAR-2002; 2002US-00091281.
XX
PA   (SIEE/) SI E.
PA   (RAYM/) RAYMOND V.
PA   (MORI/) MORISSETTE J.
XX
PI   Raymond V,  Morissette J,  Si E;
XX
DR   WPI; 2003-864168/80.
XX
PT   New nucleic acid sequences of the optineurin gene are useful to detect
PT   polymorphisms particularly single nucleotide polymorphisms in the
PT   optineurin promoter to diagnose, prognose and treat glaucoma and related
PT   disorders.
XX
PS   Claim 11; SEQ ID NO 36; 159pp; English.
XX
CC   The invention relates to an isolated nucleic acid (N1) comprising at
CC   least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC   promoter appearing as ADE13890. Also included are the optineurin promoter
CC   operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC   detecting a single nucleotide polymorphism (SNP) in the optineurin
CC   promoter, a host cell comprising the promoter operably linked to a
CC   heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC   obtained from a cell or bodily fluid (comprising detecting a polymorphism
CC   in a promoter region of the optineurin gene, associated with a glaucoma
CC   phenotype), detecting a SNP sequence variation in a sample containing
CC   DNA, detecting the presence of an optineurin promoter sequence variation
CC   in a sample containing DNA, determining the presence or increased
CC   susceptibility to glaucoma or to a progressive ocular hypertensive
CC   disorder resulting in loss of visual field in a patient (or the severity
CC   or progression of glaucoma in a patient, comprising providing
CC   amplification reaction primers that direct amplification of a selected
CC   nucleic acid region containing the variation within the optineurin
CC   promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC   obtaining a sample containing human genomic DNA, providing a nucleic acid
CC   capable of detecting a SNP located within an optineurin promoter, and
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CC   detecting the polymorphism). The invention is used to diagnose and
CC   prognose glaucoma and also to treat glaucoma related disorders. The
CC   present sequence is an optineurin promoter motif, repeat element or
CC   putative regulatory region.
XX
SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              ||||||||
Db          1 CATGGATG 8


RESULT 158
ADG98585/c
ID   ADG98585 standard; DNA; 10 BP.
XX
AC   ADG98585;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human CETP gene allele specific extension PCR primer #46.
XX
KW   human; cholesteryl ester transfer protein; CETP;
KW   single nucleotide polymorphism; SNP; drug screening; atherosclerosis;
KW   cardiovascular disease; hypercholesterolaemia;
KW   allele specific oligonucleotide; ss; extension PCR; primer.
XX
OS   Homo sapiens.
XX
PN   WO2003091277-A2.
XX
PD   06-NOV-2003.
XX
PF   28-APR-2003; 2003WO-US013288.
XX
PR   26-APR-2002; 2002US-0375791P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Chew A,  Kazemi A,  Lachowicz M,  Lee HH,  Parks KE;
PI   Petersen N,  Rounds E,  Sausker EA,  Tirrell C;
XX
DR   WPI; 2003-865576/80.
XX
PT   New isolated polynucleotide useful for haplotyping and/or genotyping
PT   cholesteryl ester transfer protein (CETP) gene in an individual or in
PT   screening for drugs useful in treating diseases associated with CETP
PT   activity.
XX
PS   Claim 45; SEQ ID NO 217; 250pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of the human
CC   cholesteryl ester transfer protein (CETP), the invention also comprises
CC   polymorphisms identified within the CETP gene. The DNA and protein
CC   sequences of the invention are useful in haplotyping and/or genotyping
CC   the CETP gene in an individual. The DNA and protein sequences may also be
CC   used to screen drugs or compounds targeting the CETP or its variant to
CC   treat a condition or disease associated with CETP (e.g. atherosclerosis,
CC   cardiovascular disease or hypercholesterolaemia). The present DNA
CC   sequence represents an allele specific extension PCR primer for the human
CC   CETP gene.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              ||||||||
Db         10 CATGGATG 3


RESULT 159
ADL96204
ID   ADL96204 standard; DNA; 10 BP.
XX
AC   ADL96204;
XX
DT   20-MAY-2004  (first entry)
XX
DE   CD15+ myeloid cell associated probe seqid 102.
XX
KW   cytostatic; gene therapy; microarray; gene expression characteristic;
KW   haematopoietic cell; haematopoiesis; myeloid leukaemia; probe;
KW   CD15+ myeloid cell; ss.
XX
OS   Homo sapiens.
XX
PN   US2003165949-A1.
XX
PD   04-SEP-2003.
XX
PF   23-DEC-2002; 2002US-00329465.
XX
PR   27-DEC-2001; 2001US-0343826P.
XX
PA   (WANG/) WANG S M.
PA   (LEES/) LEE S.
PA   (CHEN/) CHEN J.
PA   (ZHOU/) ZHOU G.
PA   (ROWL/) ROWLEY J D.
XX
PI   Wang SM,  Lee S,  Chen J,  Zhou G,  Rowley JD;
XX
DR   WPI; 2003-863699/80.
XX
PT   New microarray for measuring gene expression characteristics of
PT   hematopoietic cells, useful for preparing a composition for diagnosing or
PT   treating myeloid leukemia.
XX
PS   Claim 1; SEQ ID NO 102; 32pp; English.
XX
CC   The invention describes a microarray for measuring gene expression
CC   characteristics of haematopoietic cells comprising at least 5
CC   polynucleotides having distinct sequences. Also described are: a method
CC   of diagnosing or treating an abnormality associated with haematopoiesis;
CC   and diagnosing myeloid leukaemia in a patient. The microarray is useful
CC   for preparing a composition for diagnosing or treating myeloid leukaemia.
CC   This sequence represents a polynucleotide probe comprising a portion of
CC   an expressed gene isolated from a population of CD15+ myeloid cells and
CC   suitable for use in the microarray of the invention.
XX
SQ   Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 160
ADK72504
ID   ADK72504 standard; DNA; 10 BP.
XX
AC   ADK72504;
XX
DT   06-MAY-2004  (first entry)
XX
```

DE Human pre Cinnamomum-camphora thorin related primer, AP27.
XX
KW schizophrenia; bodily fluid; detection;
KW pre Cinnamomum-camphora thorin gene; human; ss; primer.
XX
OS Unidentified.
XX
PN JP2004024174-A.
XX
PD 29-JAN-2004.
XX
PF 27-JUN-2002; 2002JP-00188221.
XX
PR 27-JUN-2002; 2002JP-00188221.
XX
PA (NIKO-) NIPPON KOTAI KENKYUSHO KK.
XX
DR WPI; 2004-127101/13.
XX
PT Detecting tissue in fluid obtained from person suffering from
PT schizophrenia, involves detecting pre Cinnamomum-camphora thorin gene or
PT gene expressed product in fluid that binds to oligonucleotide or test
PT substance.
XX
PS Example 1; Page 79; 47pp; Japanese.
XX
CC The invention relates to a novel method for detecting an individuals
CC genetic disposition to schizophrenia by testing tissue from bodily fluid.
CC The novel method involves detecting the pre Cinnamomum-camphora thorin
CC gene or gene expressed product in the fluid that binds to
CC oligonucleotide, or test substance. The method is useful for detecting
CC tissue in a fluid obtained from a person suffering from schizophrenia.
CC This polynucleotide sequence represents a primer used in the
CC exemplification of the invention.
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCATGGTC 10
||||||||
Db 3 TCATGGTC 10

RESULT 161
ADS76364
ID ADS76364 standard; DNA; 10 BP.
XX
AC ADS76364;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #146.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
DR WPI; 2004-728732/71.
XX
PT Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 2; SEQ ID NO 146; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ATGGATGA 20
||||||||
Db 2 ATGGATGA 9

RESULT 162
ABQ87571
ID ABQ87571 standard; cDNA; 11 BP.
XX
AC ABQ87571;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 1326.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 92; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is

```
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 5 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 163
ABV67347/c
ID   ABV67347 standard; cDNA; 11 BP.
XX
AC   ABV67347;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5133.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 166; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGGTCACA 13
              ||||||||
Db          11 TGGTCACA 4


RESULT 164
ABQ78730
ID   ABQ78730 standard; RNA; 11 BP.
XX
AC   ABQ78730;
XX
DT   05-DEC-2002  (first entry)
XX
DE   Nucleotide sequence of a microsporidial rRNA gene fragment.
XX
KW   Encephalitozoon microorganism; drinking water; rRNA; ss.
XX
OS   Nosema furnacalis.
XX
PN   US2002102584-A1.
XX
PD   01-AUG-2002.
XX
PF   18-SEP-2001; 2001US-00954225.
XX
PR   21-SEP-2000; 2000US-0234241P.
XX
PA   (HEST/) HESTER J D.
PA   (LIND/) LINDQUIST H D A.
PA   (SCHA/) SCHAEFER F W.
XX
PI   Hester JD,  Lindquist HDA,  Schaefer FW;
XX
DR   WPI; 2002-673993/72.
XX
PT   New Probe for detecting Encephalitozoon protozoans e.g. Encephalitozoon
PT   cuniculi.
XX
PS   Disclosure; Page 6; 9pp; English.
XX
CC   ABQ78717-38 represent rRNA gene fragments, which were aligned to enable
CC   designing of probes of the invention. The specification describes probes
CC   specific for Encephalitozoon hellem, E. cuniculi and E. intestinalis. The
CC   probes hybridise to the 16S rRNA gene, and have a marker attached to
CC   then. The probes are able to hybridize with mRNA of one species of genus
CC   Encephalitozoon without reactivity with other microorganisms. The probes
CC   are useful for detecting the presence of Encephalitozoon microorganisms,
CC   especially Encephalitozoon hellem, Encephalitozoon cuniculi and
CC   Encephalitozoon intestinalis in drinking water
XX
SQ   Sequence 11 BP; 3 A; 2 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 86;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCACATGG 16
              :||||:||
Db          3 UCACAUGG 10


RESULT 165
ABA89952
ID   ABA89952 standard; DNA; 11 BP.
XX
AC   ABA89952;
XX
DT   11-FEB-2002  (first entry)
XX
DE   ESR-alpha gene Coriell Diversity panel oligo #32.
XX
KW   Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2;
KW   synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic;
KW   cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis;
```

```
KW   cardiovascular disease; oestrogen receptor; SNP;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(6,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200162969-A2.
XX
PD   30-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005358.
XX
PR   22-FEB-2000; 2000US-0183756P.
PR   20-OCT-2000; 2000US-00692414.
PR   24-JAN-2001; 2001US-00768184.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Kalush F,  Cassel MJ,  Hwang SS,  Winn-Deen ES;
XX
DR   WPI; 2002-041152/05.
XX
PT   Novel variant of estrogen receptor alpha polypeptide useful for
PT   determining the biological activity of a protein for high throughput
PT   screening and for raising antibodies that elicit an immune response in
PT   host.
XX
PS   Claim 17; Fig 2b sheet 2; 333pp; English.
XX
CC   The present invention describes an isolated peptide (I) consisting of an
CC   amino acid sequence selected from: (a) the amino acid sequence of a
CC   variant of the oestrogen receptor alpha (ESR-alpha) protein in AAG68251;
CC   or (b) a fragment comprising at least 10 contiguous amino acids of the
CC   protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and
CC   vasotropic activities, and can be used in gene therapy and vaccine
CC   production. (I) is useful for identifying an agent that binds to (I), by
CC   contacting (I) with an agent and assaying the contacted mixture to
CC   determine whether a complex is formed with the agent bound to the
CC   peptide. A polynucleotide (II), encoding (I), is useful in the
CC   development of diagnostics and therapies for diseases and disorders
CC   mediated/modulated by an oestrogen receptor (ER). (II) is also useful in
CC   gene therapy for treating cancer, osteoporosis and cardiovascular
CC   diseases. The human ESR-alpha gene is located on chromosome 6. ABA89869
CC   to ABA89972 represent ESR-alpha gene single nucleotide polymorphism (SNP)
CC   containing oligonucleotides, which are used in an example from the
CC   present invention
XX
SQ   Sequence 11 BP; 4 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              ||||||||
Db          1 CATGGATG 8


RESULT 166
ABA89900
ID   ABA89900 standard; DNA; 11 BP.
XX
AC   ABA89900;
XX
DT   11-FEB-2002  (first entry)
XX
DE   ESR-alpha gene Liverpool clinical tissue sample SNP oligo #32.
XX
KW   Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2;
KW   synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic;
KW   cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis;
KW   cardiovascular disease; oestrogen receptor; SNP;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(6,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200162969-A2.
XX
PD   30-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005358.
XX
PR   22-FEB-2000; 2000US-0183756P.
PR   20-OCT-2000; 2000US-00692414.
PR   24-JAN-2001; 2001US-00768184.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Kalush F,  Cassel MJ,  Hwang SS,  Winn-Deen ES;
XX
DR   WPI; 2002-041152/05.
XX
PT   Novel variant of estrogen receptor alpha polypeptide useful for
PT   determining the biological activity of a protein for high throughput
PT   screening and for raising antibodies that elicit an immune response in
PT   host.
XX
PS   Claim 17; Fig 2a sheet 2; 333pp; English.
XX
CC   The present invention describes an isolated peptide (I) consisting of an
CC   amino acid sequence selected from: (a) the amino acid sequence of a
CC   variant of the oestrogen receptor alpha (ESR-alpha) protein in AAG68251;
CC   or (b) a fragment comprising at least 10 contiguous amino acids of the
CC   protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and
CC   vasotropic activities, and can be used in gene therapy and vaccine
CC   production. (I) is useful for identifying an agent that binds to (I), by
CC   contacting (I) with an agent and assaying the contacted mixture to
CC   determine whether a complex is formed with the agent bound to the
CC   peptide. A polynucleotide (II), encoding (I), is useful in the
CC   development of diagnostics and therapies for diseases and disorders
CC   mediated/modulated by an oestrogen receptor (ER). (II) is also useful in
CC   gene therapy for treating cancer, osteoporosis and cardiovascular
CC   diseases. The human ESR-alpha gene is located on chromosome 6. ABA89869
CC   to ABA89972 represent ESR-alpha gene single nucleotide polymorphism (SNP)
CC   containing oligonucleotides, which are used in an example from the
CC   present invention
XX
SQ   Sequence 11 BP; 4 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              ||||||||
Db          1 CATGGATG 8


RESULT 167
ABK99375
ID   ABK99375 standard; DNA; 11 BP.
XX
AC   ABK99375;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human CYP3A5 gene polymorphic reference DNA sequence #15.
```

XX
KW Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW AIDS; African American; forensic marker; pharmacological; cytostatic;
KW antidiabetic; anti-HIV; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200253775-A2.
XX
PD 11-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-EP015290.
XX
PR 28-DEC-2000; 2000EP-00128627.
PR 28-DEC-2000; 2000US-0258684P.
PR 29-DEC-2000; 2000US-0258952P.
PR 16-JAN-2001; 2001EP-00100172.
PR 18-JAN-2001; 2001US-0262859P.
PR 16-AUG-2001; 2001EP-00118884.
PR 16-AUG-2001; 2001US-0312825P.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Haberl M, Hustert E;
XX
DR WPI; 2002-583628/62.
XX
PT Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT cardiovascular diseases, diabetes and AIDS, and for identifying
PT polymorphisms.
XX
PS Example 2; Page 48; 138pp; English.
XX
CC The present invention relates to a new CYP3A5 polynucleotide encoding a
CC polypeptide, where the polynucleotide is capable of hybridising to a
CC CYP3A5 gene. The invention is useful in an in vitro method for
CC identifying a polymorphism. The invention is also useful for useful for
CC diagnosing a disorder related to the presence of a molecular variant of a
CC CYP3A5 or susceptibility to such a disorder, where the disorder is
CC cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC The invention can further be used for the preparation of a diagnostic
CC composition for diagnosing a disease in a subject having a genome
CC comprising a variant allele of the CYP3A5 gene, where the subject is an
CC African American. The molecules of the invention are as forensic markers
CC and in pharmacological studies. The present nucleic acid sequence
CC represents a human CYP3A5 gene polymorphism reference DNA sequence, as
CC described in the invention
XX
SQ Sequence 11 BP; 4 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CACATGGA 17
||||||||
Db 4 CACATGGA 11

RESULT 168
ABK99363/c
ID ABK99363 standard; DNA; 11 BP.
XX
AC ABK99363;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human CYP3A5 gene polymorphic reference DNA sequence #9.
XX
KW Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW AIDS; African American; forensic marker; pharmacological; cytostatic;
KW antidiabetic; anti-HIV; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200253775-A2.
XX
PD 11-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-EP015290.
XX
PR 28-DEC-2000; 2000EP-00128627.
PR 28-DEC-2000; 2000US-0258684P.
PR 29-DEC-2000; 2000US-0258952P.
PR 16-JAN-2001; 2001EP-00100172.
PR 18-JAN-2001; 2001US-0262859P.
PR 16-AUG-2001; 2001EP-00118884.
PR 16-AUG-2001; 2001US-0312825P.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Haberl M, Hustert E;
XX
DR WPI; 2002-583628/62.
XX
PT Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT cardiovascular diseases, diabetes and AIDS, and for identifying
PT polymorphisms.
XX
PS Example 2; Page 48; 138pp; English.
XX
CC The present invention relates to a new CYP3A5 polynucleotide encoding a
CC polypeptide, where the polynucleotide is capable of hybridising to a
CC CYP3A5 gene. The invention is useful in an in vitro method for
CC identifying a polymorphism. The invention is also useful for useful for
CC diagnosing a disorder related to the presence of a molecular variant of a
CC CYP3A5 or susceptibility to such a disorder, where the disorder is
CC cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC The invention can further be used for the preparation of a diagnostic
CC composition for diagnosing a disease in a subject having a genome
CC comprising a variant allele of the CYP3A5 gene, where the subject is an
CC African American. The molecules of the invention are as forensic markers
CC and in pharmacological studies. The present nucleic acid sequence
CC represents a human CYP3A5 gene polymorphism reference DNA sequence, as
CC described in the invention
XX
SQ Sequence 11 BP; 4 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 ACATGGAT 18
||||||||
Db 8 ACATGGAT 1

RESULT 169
ADQ30150/c
ID ADQ30150 standard; DNA; 11 BP.
XX
AC ADQ30150;
XX
DT 09-SEP-2004 (first entry)
XX
DE Murine VR1 exon 1d transcription factor binding fragment #42.
XX
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;
KW detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;
KW hypalgesia; hyperalgesia; neuralgia; myalgia; murine.
XX
OS Mus sp.
XX
PN WO2004053120-A2.
XX

PD 24-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-EP013522.
XX
PR 09-DEC-2002; 2002DE-01057421.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Weihe E, Bieller A, Schaefer MKH;
XX
DR WPI; 2004-468868/44.
XX
PT New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX
PS Disclosure; Page 49; 68pp; German.
XX
CC This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VR1
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridises to it under
CC standard conditions. The VR1 modulator is derived from one or more of
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VR1 modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VR1 receptor by introducing the
CC modulator or the vector into a cell that contains the VR1 gene. The
CC products of the invention are used for detecting a transcription factor
CC from its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbant assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VR1 receptor expression includes a
CC binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or
CC GATA1. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC neuralgia and myalgia, that are associated with activity of the VR1
CC receptor. This sequence represents a fragment of murine VR1 exon 1d DNA
CC which is capable of binding to a transcription factor.
XX
SQ Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 ATGGTCAC 12
              ||||||||
Db          9 ATGGTCAC 2
```

RESULT 170
ADZ23297
ID ADZ23297 standard; DNA; 11 BP.
XX
AC ADZ23297;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human SNP detection related oligonucelotide #264.
XX
KW ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
KW immune disorder; cardiovascular disease; metabolic disorder;
KW respiratory disease; musculoskeletal disease; renal disease;
KW nephrotropic; endocrine disease; genitourinary disease.
XX
OS Homo sapiens.
XX
PN WO2005030952-A1.
XX
PD 07-APR-2005.
XX
PF 30-SEP-2004; 2004WO-JP014784.
XX
PR 30-SEP-2003; 2003JP-00342519.
PR 28-MAY-2004; 2004JP-00158717.
XX
PA (RIKE) RIKEN KK.
PA (STAG-) STAGEN CO LTD.
PA (SEKI/) SEKINE A.
PA (IIDA/) IIDA A.
PA (SAIT/) SAITO S.
XX
PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;
XX
DR WPI; 2005-305936/31.
XX
PT Analyzing haplotype, by detecting polymorphism in drug-related genes,
PT electing common polymorphism (CP), building haplotype block using CP,
PT specifying CP within block, specifying tag polymorphism from CP within
PT block.
XX
PS Disclosure; SEQ ID NO 264; 1290pp; Japanese.
XX
CC The invention relates to a method of analyzing haplotype, by detecting
CC gene polymorphism in drug-related genes such as aryl acetylamide
CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
CC sub-family A (ABC1), member 1. The method is useful for analyzing
CC haplotype. The method is useful for estimating the sensitivity or disease
CC of a medicine or a foreign material, for selecting medicine for
CC preventing or treating diseases, for determining appropriate dosage of
CC medicine for preventing or treating a disease, for analyzing a drug
CC interaction, and for determining the related polymorphism relative to the
CC sensitivity of the medicine, foreign material or disease. The diseases
CC include malignant tumor, immune disorder circulatory disease, metabolic
CC disease, kidney disease, respiratory disease and muscle associated
CC disease. The method enables analysis of the individual differences
CC related to the sensitivity of a medicine, using a haplotype, without
CC using each single nucleotide polymorphism. The present sequence
CC represents a human SNP detection related oligonucelotide.
XX
SQ Sequence 11 BP; 3 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 GGTCACAT 14
              ||||||||
Db          1 GGTCACAT 8
```

RESULT 171
AAX32604
ID AAX32604 standard; DNA; 11 BP.
XX
AC AAX32604;
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #4.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.

```
XX
PR   28-FEB-1994;   94US-00202927.
XX
PA   (MICR-) MICROPROBE CORP.
PA   (UYYA ) UNIV YALE.
XX
PI   Cheng Y,  Lukhtanov EA,  Meyer RB,  Pai BS,  Reed MW,  Zhou JH;
XX
DR   WPI; 1995-311501/40.
XX
PT   New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT   intramolecular duplex with hairpin loop region, having selective
PT   cytotoxicity against some tumour cells.
XX
PS   Disclosure; Page 46; 107pp; English.
XX
CC   New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC   and which have a steroid structure attached to the 3'-end through a
CC   linker attached to the A-ring of the steroid skeleton. In particular, the
CC   present sequence has a cholesterol moiety attached by its A-ring to to
CC   the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC   of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC   oligonucleotides form stable duplexes at physiological temperature and
CC   have selective cytotoxic activity against certain tumour cell lines,
CC   including some with multiple drug resistance
XX
SQ   Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          10 CACATGGATGA 20
               |||| || |||
Db           1 CACACGGGTGA 11


RESULT 172
AAZ18893
ID   AAZ18893 standard; DNA; 11 BP.
XX
AC   AAZ18893;
XX
DT   22-OCT-1999  (first entry)
XX
DE   Murine MRL SAGE tag 1931794.
XX
KW   Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW   healing response; microsatellite marker; treatment; central nerve;
KW   peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
OS   Mus sp.
XX
PN   WO9941364-A2.
XX
PD   19-AUG-1999.
XX
PF   12-FEB-1999;   99WO-US002962.
XX
PR   13-FEB-1998;   98US-0074737P.
PR   26-AUG-1998;   98US-0097937P.
PR   28-SEP-1998;   98US-0102051P.
XX
PA   (WIST-) WISTAR INST.
XX
PI   Heber-Katz E;
XX
DR   WPI; 1999-494533/41.
XX
PT   New mammalian model for enhanced wound healing - useful for identifying
PT   enhanced wound healing genes.
XX
PS   Claim 13; Page 72; 136pp; English.
XX
CC   This invention describes a novel non-MRL healer mouse (M) having at least
CC   one quantitative trait locus selected from those given in the
CC   specification, exhibiting an enhanced healing response to a wound
CC   compared to mice (m) without the locus. The invention describes a novel
CC   method of identifying a gene involved in enhanced wound healing by
CC   identifying DNA microsatellite markers which can distinguish healer mice
CC   from non-healer mice and identifying microsatellite markers which
CC   segregate with enhanced wound healing in progeny of the mice, where a
CC   chromosomal locus containing at least one enhanced wound healing gene is
CC   identified. A method of treating a wound in a mammal is also disclosed.
CC   The new methods are useful for treating wounds, especially central and
CC   peripheral nerve wound. The methods of the invention are useful for
CC   restoring function after nerve injury in a mammal. (M) is useful as a
CC   mammalian model of enhanced wound healing, useful for identifying genes
CC   and gene products involved in enhanced wound healing, and to provide
CC   methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC   from C57BL/6 and MRL mice which are used to illustrate the method of the
CC   invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           2 CTCATGGTCAC 12
               ||| ||| |||
Db           1 CTCCTGGACAC 11


RESULT 173
AAZ18751
ID   AAZ18751 standard; DNA; 11 BP.
XX
AC   AAZ18751;
XX
DT   22-OCT-1999  (first entry)
XX
DE   Murine C57BL/6 SAGE tag 1931794.
XX
KW   Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW   healing response; microsatellite marker; treatment; central nerve;
KW   peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
OS   Mus sp.
XX
PN   WO9941364-A2.
XX
PD   19-AUG-1999.
XX
PF   12-FEB-1999;   99WO-US002962.
XX
PR   13-FEB-1998;   98US-0074737P.
PR   26-AUG-1998;   98US-0097937P.
PR   28-SEP-1998;   98US-0102051P.
XX
PA   (WIST-) WISTAR INST.
XX
PI   Heber-Katz E;
XX
DR   WPI; 1999-494533/41.
XX
PT   New mammalian model for enhanced wound healing - useful for identifying
PT   enhanced wound healing genes.
XX
PS   Claim 13; Page 56; 136pp; English.
XX
CC   This invention describes a novel non-MRL healer mouse (M) having at least
CC   one quantitative trait locus selected from those given in the
CC   specification, exhibiting an enhanced healing response to a wound
CC   compared to mice (m) without the locus. The invention describes a novel
CC   method of identifying a gene involved in enhanced wound healing by
```

```
CC   identifying DNA microsatellite markers which can distinguish healer mice
CC   from non-healer mice and identifying microsatellite markers which
CC   segregate with enhanced wound healing in progeny of the mice, where a
CC   chromosomal locus containing at least one enhanced wound healing gene is
CC   identified. A method of treating a wound in a mammal is also disclosed.
CC   The new methods are useful for treating wounds, especially central and
CC   peripheral nerve wound. The methods of the invention are useful for
CC   restoring function after nerve injury in a mammal. (M) is useful as a
CC   mammalian model of enhanced wound healing, useful for identifying genes
CC   and gene products involved in enhanced wound healing, and to provide
CC   methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC   from C57BL/6 and MRL mice which are used to illustrate the method of the
CC   invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||| ||| |||
Db          1 CTCCTGGACAC 11


RESULT 174
ABV67178/c
ID   ABV67178 standard; cDNA; 11 BP.
XX
AC   ABV67178;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4964.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 162; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              |||  ||||||
Db         11 TCAGTGTCACA 1


RESULT 175
ABV62315
ID   ABV62315 standard; cDNA; 11 BP.
XX
AC   ABV62315;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 101.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 28; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CACATGGATGA 20
              |||| ||| ||
Db          1 CACAGGGAGGA 11


RESULT 176
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```
ABV66218
ID   ABV66218 standard; cDNA; 11 BP.
XX
AC   ABV66218;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4004.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 136; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              |||  ||||||
Db          1 CATATTCACAT 11


RESULT 177
ABV64369
ID   ABV64369 standard; cDNA; 11 BP.
XX
AC   ABV64369;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2155.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 85; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              |||  ||||||
Db          1 CATCGTTACAT 11


RESULT 178
ABV63523
ID   ABV63523 standard; cDNA; 11 BP.
XX
AC   ABV63523;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 1309.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
```

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XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 61; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 TCACATGGATG 19
              ||||| || ||
Db          1 TCACAAGGCTG 11


RESULT 179
ABV66979
ID   ABV66979 standard; cDNA; 11 BP.
XX
AC   ABV66979;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4765.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 156; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATG 15
              |||||| | ||
Db          1 ATGGTCTCCTG 11


RESULT 180
ABV70944
ID   ABV70944 standard; cDNA; 11 BP.
XX
AC   ABV70944;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8730.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 280; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
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  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 TCACATGGATG 19
              ||||| || ||
Db          1 TCACAAGGCTG 11


RESULT 181
ABV66624
ID   ABV66624 standard; cDNA; 11 BP.
XX
AC   ABV66624;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4410.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 146; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCA 11
              || | ||||||
Db          1 CCCCGTGGTCA 11


RESULT 182
ABV67607
ID   ABV67607 standard; cDNA; 11 BP.
XX
AC   ABV67607;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5393.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 174; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              || |||||| |
Db          1 CTTATGGTCCC 11


RESULT 183
ABV71790
ID   ABV71790 standard; cDNA; 11 BP.
XX
AC   ABV71790;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9576.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
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XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 309; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              ||| || ||||
Db          1 CATCGTTACAT 11


RESULT 184
ABV65780/c
ID   ABV65780 standard; cDNA; 11 BP.
XX
AC   ABV65780;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3566.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 124; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGG 16
              || ||| ||||
Db         11 TGATCATATGG 1


RESULT 185
ABV69736
ID   ABV69736 standard; cDNA; 11 BP.
XX
AC   ABV69736;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7522.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 237; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
```

```
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CACATGGATGA 20
                ||||  ||| ||
Db          1 CACAGGGAGGA 11


RESULT 186
ADA44629/c
ID   ADA44629 standard; DNA; 11 BP.
XX
AC   ADA44629;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Avian beta-defensin GAL1/THP1 prepro peptide initiation sequence.
XX
KW   ds; chicken; GAL1; beta-defensin; avian; infection; microbe; bacterium;
KW   virus; protozoa; fungus; veterinary use; turkey; THP1.
XX
OS   Gallus gallus.
OS   Meleagris gallopavo.
XX
PN   US6545140-B1.
XX
PD   08-APR-2003.
XX
PF   13-JUL-1999;   99US-00351657.
XX
PR   13-JUL-1998;   98US-0092668P.
XX
PA   (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI   Harmon BG,  Jackwood MW,  Brockus CW;
XX
DR   WPI; 2003-566588/53.
XX
PT   New isolated and purified nucleic acid molecule encoding prepro form of
PT   Turkey heterophil peptide 2 which is an avian beta-defensin polypeptide,
PT   useful for treating or preventing microbial infection in avians.
XX
PS   Example 1; Col 27; 40pp; English.
XX
CC   The invention relates to an isolated and purified nucleic acid molecule
CC   comprising a Meleagris gallopavo nucleic acid sequence which encodes
CC   prepro beta-defensin polypeptide turkey heterophil peptide 2 (THP2). The
CC   nucleic acid is useful for expressing an avian beta defensin polypeptide,
CC   preferably THP2 peptide. The THP2 peptide is useful for treating,
CC   inhibiting, reducing or preventing a microbial (bacterial, viral,
CC   protozoal or fungal) infection in avians and mammals for veterinary use
CC   such as for use with domestic or farm animals. The present sequence
CC   represents the avian beta-defensin GAL2/THP2 prepro peptide initiation
CC   sequence.
XX
SQ   Sequence 11 BP; 5 A; 2 C; 2 G; 0 T; 2 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
                ||||||  |||
Db         11 CATGGTTTCAT 1


RESULT 187
ADK13996
ID   ADK13996 standard; DNA; 11 BP.
XX
AC   ADK13996;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human methyl-CpG-binding protein 2, MECP2, mutation #5.
XX
KW   human; Rett syndrome; methyl-CpG-binding protein 2; MECP2;
KW   neurodevelopmental disease; autism; non-syndromic mental retardation;
KW   idiopathic neonatal encephalopathy; idiopathic infantile spasm;
KW   idiopathic cerebral palsy; Angelman syndrome; schizophrenia; ds.
XX
OS   Homo sapiens.
XX
PN   US6709817-B1.
XX
PD   23-MAR-2004.
XX
PF   07-SEP-2000; 2000US-00657013.
XX
PR   07-SEP-1999;   99US-0152778P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Zoghbi HY,  Van Den Veyver IB,  Amir R,  Francke U;
XX
DR   WPI; 2004-256068/24.
XX
PT   Screening human for Rett syndrome comprises detecting mutation in nucleic
PT   acid sequence encoding methyl-CpG-binding protein 2 (MECP2).
XX
PS   Disclosure; SEQ ID NO 98; 125pp; English.
XX
CC   The invention relates to a method of screening a human for Rett syndrome
CC   comprising detecting a mutation in a nucleic acid sequence encoding
CC   methyl-CpG-binding protein 2 (MECP2). The method is useful for screening
CC   a human for Rett syndrome. The method is useful for screening
CC   neurodevelopmental diseases such as Rett syndrome, autism, non-syndromic
CC   mental retardation, idiopathic neonatal encephalopathy, idiopathic
CC   infantile spasms, idiopathic cerebral palsy, Angelman syndrome and
CC   schizophrenia. The present sequence represents a mutation in the human
CC   methyl-CpG-binding protein 2, MECP2, DNA
XX
SQ   Sequence 11 BP; 3 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCA 11
                | |||||||  |
Db          1 CTTCATGGTAA 11


RESULT 188
ADQ35891/c
ID   ADQ35891 standard; DNA; 11 BP.
XX
AC   ADQ35891;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human hair-bearing skin-associated DNA fragment SEQ ID NO 708.
XX
KW   hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260931-A1.
```

XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060931.
XX
PR 20-DEC-2002; 2002DE-01060931.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518857/50.
XX
PT In vitro identification of genes important for hair-bearing skin, useful
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 5; SEQ ID NO 708; 250pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for hair-bearing skin in humans. The method
CC comprises recovering, from hair-bearing skin, a first mixture of
CC genetically expressed (transcribed and optionally translated) factors
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC mixture from skin on which hair does not grow and subjecting both
CC mixtures to serial analysis of gene expression (SAGE) to identify those
CC genes for which expression is markedly different between the two types of
CC skin. The invention also describes in vitro methods for determining
CC homeostasis of human hair-bearing skin and for determining activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC a test kit comprising a solid support (flexible or rigid) with
CC immobilised probes are also described for determining homeostasis. The
CC hair-bearing skin is from the scalp and the other skin is from the face.
CC The method allows identification of as many as possible of the genes
CC important for hair-bearing skin, and therefore, of a very wide range of
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC human DNA Tag fragments used to identify genes associated with hair-
CC bearing skin.
XX
SQ Sequence 11 BP; 4 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 TCATGGTCACA 13
              || |||| |||
Db         11 TCTTGGTAACA 1
```

RESULT 189
ADQ35434
ID ADQ35434 standard; DNA; 11 BP.
XX
AC ADQ35434;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 251.
XX
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS Homo sapiens.
XX
PN DE10260931-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060931.
XX
PR 20-DEC-2002; 2002DE-01060931.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518857/50.
XX
PT In vitro identification of genes important for hair-bearing skin, useful
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 6; SEQ ID NO 251; 250pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for hair-bearing skin in humans. The method
CC comprises recovering, from hair-bearing skin, a first mixture of
CC genetically expressed (transcribed and optionally translated) factors
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC mixture from skin on which hair does not grow and subjecting both
CC mixtures to serial analysis of gene expression (SAGE) to identify those
CC genes for which expression is markedly different between the two types of
CC skin. The invention also describes in vitro methods for determining
CC homeostasis of human hair-bearing skin and for determining activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC a test kit comprising a solid support (flexible or rigid) with
CC immobilised probes are also described for determining homeostasis. The
CC hair-bearing skin is from the scalp and the other skin is from the face.
CC The method allows identification of as many as possible of the genes
CC important for hair-bearing skin, and therefore, of a very wide range of
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC human DNA Tag fragments used to identify genes associated with hair-
CC bearing skin.
XX
SQ Sequence 11 BP; 3 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 CATGGTCACAT 14
              ||| || ||||
Db          1 CATCGTTACAT 11
```

RESULT 190
ADQ35336/c
ID ADQ35336 standard; DNA; 11 BP.
XX
AC ADQ35336;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 153.
XX
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS Homo sapiens.
XX
PN DE10260931-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060931.
XX
PR 20-DEC-2002; 2002DE-01060931.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;

```
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518857/50.
XX
PT   In vitro identification of genes important for hair-bearing skin, useful
PT   for assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 6; SEQ ID NO 153; 250pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for hair-bearing skin in humans. The method
CC   comprises recovering, from hair-bearing skin, a first mixture of
CC   genetically expressed (transcribed and optionally translated) factors
CC   (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC   mixture from skin on which hair does not grow and subjecting both
CC   mixtures to serial analysis of gene expression (SAGE) to identify those
CC   genes for which expression is markedly different between the two types of
CC   skin. The invention also describes in vitro methods for determining
CC   homeostasis of human hair-bearing skin and for determining activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC   a test kit comprising a solid support (flexible or rigid) with
CC   immobilised probes are also described for determining homeostasis. The
CC   hair-bearing skin is from the scalp and the other skin is from the face.
CC   The method allows identification of as many as possible of the genes
CC   important for hair-bearing skin, and therefore, of a very wide range of
CC   potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC   human DNA Tag fragments used to identify genes associated with hair-
CC   bearing skin.
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||| ||||||
Db         11 TCAGTGTCACA 1


RESULT 191
ADQ34440
ID   ADQ34440 standard; DNA; 11 BP.
XX
AC   ADQ34440;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 2530.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 4; SEQ ID NO 2530; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATG 15
              |||||| | ||
Db          1 ATGGTCTCCTG 11


RESULT 192
ADW11578/c
ID   ADW11578 standard; RNA; 12 BP.
XX
AC   ADW11578;
XX
DT   24-MAR-2005  (first entry)
XX
DE   siRNA production-related p4 box RNA SeqID15.
XX
KW   short interfering RNA; siRNA; RNA interference; ribozyme; ss.
XX
OS   Unidentified.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .4
FT                   /*tag=  b
FT                   /bound_moiety= "Itself"
FT                   /note= "Binds nucleotides 12-9 of itself"
FT   misc_binding    9. .12
FT                   /*tag=  b
FT                   /bound_moiety= "Itself"
FT                   /note= "Binds nucleotides 4-1 of itself"
XX
PN   WO2005001039-A2.
XX
PD   06-JAN-2005.
XX
PF   28-MAY-2004; 2004WO-US017034.
XX
PR   29-MAY-2003; 2003US-0474001P.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
```

PI Soukup GA, Kertsburg A;
XX
DR WPI; 2005-075534/08.
XX
PT Producing a small, interfering RNA (siRNA) by providing a first or second
PT RNA construct comprising a first or second ribozyme operably linked to a
PT sense or an antisense strand, respectively of an siRNA.
XX
PS Example 1; SEQ ID NO 15; 43pp; English.
XX
CC This invention relates to a novel method of producing a small interfering
CC RNA (siRNA). The method comprises providing a first RNA construct
CC comprising a first ribozyme operably linked to a sense and antisense
CC strand of an siRNA and placing the first and second RNA constructs under
CC conditions where the first and second ribozyme catalyze the cleavage of
CC the sense and antisense strands of the siRNA from the first and second
CC RNA constructs. The present sequence is that of a p4 box RNA which was
CC used during the exemplification of the method of the invention.
XX
SQ Sequence 12 BP; 5 A; 2 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 36.0%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 CATGGTCACATG 15
              |||| |  ||||
Db         12 CATGTTTCCATG 1
```

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Job time : 1 secs

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OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 13:56:07 ; Search time 0.001 Seconds
(without alignments)
69.960 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 160 seqs, 1749 residues

Total number of hits satisfying chosen parameters: 320

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 163 summaries

Database : rge.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	85.0	20	1	CS097426	ACCESSION:CS097426
	2	14.8	74.0	19	1	AR199401	ACCESSION:AR199401
c	3	12.8	64.0	17	1	AX732438	ACCESSION:AX732438
c	4	12.2	61.0	17	1	CQ622872	ACCESSION:CQ622872
c	5	12.2	61.0	17	1	AR463935	ACCESSION:AR463935
	6	10.8	54.0	15	1	AR180445	ACCESSION:AR180445
c	7	9.4	47.0	11	1	CQ828639	ACCESSION:CQ828639
	8	9.4	47.0	12	1	A71522	ACCESSION:A71522
	9	9.4	47.0	12	1	S74610	ACCESSION:S74610
	10	9.4	47.0	13	1	AR759769	ACCESSION:AR759769
c	11	9.4	47.0	13	1	AR759770	ACCESSION:AR759770
c	12	9	45.0	11	1	BD124291	ACCESSION:BD124291
c	13	9	45.0	11	1	AR301541	ACCESSION:AR301541
	14	9	45.0	11	1	AX472166	ACCESSION:AX472166
c	15	9	45.0	12	1	AR058623	ACCESSION:AR058623
	16	8.8	44.0	12	1	I04322	ACCESSION:I04322
	17	8.4	42.0	10	1	A04966	ACCESSION:A04966
c	18	8.4	42.0	10	1	BD166495	ACCESSION:BD166495
c	19	8.4	42.0	10	1	BD167034	ACCESSION:BD167034
c	20	8.4	42.0	10	1	CQ858077	ACCESSION:CQ858077
	21	8.4	42.0	10	1	AR194807	ACCESSION:AR194807
	22	8.4	42.0	10	1	I54941	ACCESSION:I54941
	23	8.4	42.0	10	1	I54945	ACCESSION:I54945
	24	8.4	42.0	10	1	AR562123	ACCESSION:AR562123
	25	8.4	42.0	10	1	AR567221	ACCESSION:AR567221
	26	8.4	42.0	10	1	AR567927	ACCESSION:AR567927
	27	8.4	42.0	10	1	AR577802	ACCESSION:AR577802
	28	8.4	42.0	10	1	AR580135	ACCESSION:AR580135
	29	8.4	42.0	10	1	AR614595	ACCESSION:AR614595
	30	8.4	42.0	10	1	AR652778	ACCESSION:AR652778
	31	8.4	42.0	10	1	AR659094	ACCESSION:AR659094
	32	8.4	42.0	10	1	AX152149	ACCESSION:AX152149
	33	8.4	42.0	11	1	CQ835676	ACCESSION:CQ835676
c	34	8.4	42.0	11	1	CQ835701	ACCESSION:CQ835701
c	35	8.4	42.0	11	1	CQ835852	ACCESSION:CQ835852
	36	8.4	42.0	11	1	AX470966	ACCESSION:AX470966
	37	8.4	42.0	11	1	AX624145	ACCESSION:AX624145
c	38	8.4	42.0	11	1	AX625704	ACCESSION:AX625704
c	39	8.4	42.0	11	1	AX626419	ACCESSION:AX626419
	40	8.4	42.0	11	1	AX631566	ACCESSION:AX631566
c	41	8.4	42.0	12	1	AR024074	ACCESSION:AR024074
c	42	8.4	42.0	12	1	AR075457	ACCESSION:AR075457
c	43	8.4	42.0	12	1	AR108947	ACCESSION:AR108947
c	44	8.4	42.0	12	1	AR153908	ACCESSION:AR153908
c	45	8.4	42.0	12	1	AR172244	ACCESSION:AR172244
c	46	8.4	42.0	12	1	AR178525	ACCESSION:AR178525
c	47	8.4	42.0	12	1	BD001178	ACCESSION:BD001178
c	48	8.4	42.0	12	1	BD001607	ACCESSION:BD001607
c	49	8.4	42.0	12	1	BD064941	ACCESSION:BD064941
c	50	8.4	42.0	12	1	BD240723	ACCESSION:BD240723
	51	8.4	42.0	12	1	BD261806	ACCESSION:BD261806
	52	8.4	42.0	12	1	CQ828540	ACCESSION:CQ828540
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c	55	8.4	42.0	12	1	AR234464	ACCESSION:AR234464
c	56	8.4	42.0	12	1	AR275829	ACCESSION:AR275829
c	57	8.4	42.0	12	1	I58612	ACCESSION:I58612
c	58	8.4	42.0	12	1	I72395	ACCESSION:I72395
	59	8.4	42.0	12	1	AR577337	ACCESSION:AR577337
	60	8.4	42.0	12	1	AR699868	ACCESSION:AR699868
	61	8.4	42.0	12	1	AR699877	ACCESSION:AR699877
c	62	8.4	42.0	12	1	AR699878	ACCESSION:AR699878
	63	8.4	42.0	12	1	AX283286	ACCESSION:AX283286
c	64	8.4	42.0	12	1	AX711060	ACCESSION:AX711060
	65	8	40.0	10	1	A41398	ACCESSION:A41398
c	66	8	40.0	10	1	AR030211	ACCESSION:AR030211
	67	8	40.0	10	1	BD083377	ACCESSION:BD083377
	68	8	40.0	10	1	BD238706	ACCESSION:BD238706
	69	8	40.0	10	1	BD240099	ACCESSION:BD240099
	70	8	40.0	10	1	I22203	ACCESSION:I22203
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	72	8	40.0	11	1	BD106575	ACCESSION:BD106575
c	73	8	40.0	11	1	CQ828725	ACCESSION:CQ828725
	74	8	40.0	11	1	CS058623	ACCESSION:CS058623
	75	8	40.0	11	1	AR636603	ACCESSION:AR636603
	76	8	40.0	11	1	AX471749	ACCESSION:AX471749
c	77	8	40.0	11	1	AX472076	ACCESSION:AX472076
	78	8	40.0	11	1	AX472088	ACCESSION:AX472088
c	79	8	40.0	11	1	AX628092	ACCESSION:AX628092
	80	7.8	39.0	11	1	BD124230	ACCESSION:BD124230
	81	7.8	39.0	11	1	BD124372	ACCESSION:BD124372
c	82	7.8	39.0	11	1	CQ832782	ACCESSION:CQ832782
	83	7.8	39.0	11	1	CQ832880	ACCESSION:CQ832880
c	84	7.8	39.0	11	1	CQ833337	ACCESSION:CQ833337
	85	7.8	39.0	11	1	CQ837472	ACCESSION:CQ837472
c	86	7.8	39.0	11	1	CS058638	ACCESSION:CS058638
	87	7.8	39.0	11	1	AR301480	ACCESSION:AR301480
	88	7.8	39.0	11	1	AR301622	ACCESSION:AR301622
c	89	7.8	39.0	11	1	AR305523	ACCESSION:AR305523
	90	7.8	39.0	11	1	I54914	ACCESSION:I54914
	91	7.8	39.0	11	1	AR488869	ACCESSION:AR488869
	92	7.8	39.0	11	1	AX623060	ACCESSION:AX623060
	93	7.8	39.0	11	1	AX624268	ACCESSION:AX624268
	94	7.8	39.0	11	1	AX625114	ACCESSION:AX625114
c	95	7.8	39.0	11	1	AX626525	ACCESSION:AX626525
	96	7.8	39.0	11	1	AX626963	ACCESSION:AX626963
	97	7.8	39.0	11	1	AX627369	ACCESSION:AX627369
	98	7.8	39.0	11	1	AX627724	ACCESSION:AX627724
c	99	7.8	39.0	11	1	AX627923	ACCESSION:AX627923
	100	7.8	39.0	11	1	AX628352	ACCESSION:AX628352
	101	7.8	39.0	11	1	AX630481	ACCESSION:AX630481
	102	7.8	39.0	11	1	AX631689	ACCESSION:AX631689
	103	7.8	39.0	11	1	AX632535	ACCESSION:AX632535
c	104	7.4	37.0	9	1	AX669046	ACCESSION:AX669046
c	105	7.4	37.0	9	1	AX669047	ACCESSION:AX669047
c	106	7.4	37.0	10	1	AR004936	ACCESSION:AR004936

c 107	7.4	37.0	10	1	AR036563	ACCESSION:AR036563
c 108	7.4	37.0	10	1	BD007825	ACCESSION:BD007825
c 109	7.4	37.0	10	1	BD065345	ACCESSION:BD065345
c 110	7.4	37.0	10	1	BD091128	ACCESSION:BD091128
c 111	7.4	37.0	10	1	BD161260	ACCESSION:BD161260
c 112	7.4	37.0	10	1	BD161382	ACCESSION:BD161382
c 113	7.4	37.0	10	1	BD166523	ACCESSION:BD166523
c 114	7.4	37.0	10	1	BD166590	ACCESSION:BD166590
c 115	7.4	37.0	10	1	BD166762	ACCESSION:BD166762
c 116	7.4	37.0	10	1	BD167122	ACCESSION:BD167122
c 117	7.4	37.0	10	1	BD167240	ACCESSION:BD167240
c 118	7.4	37.0	10	1	BD167877	ACCESSION:BD167877
c 119	7.4	37.0	10	1	BD238612	ACCESSION:BD238612
c 120	7.4	37.0	10	1	BD239861	ACCESSION:BD239861
c 121	7.4	37.0	10	1	BD240651	ACCESSION:BD240651
c 122	7.4	37.0	10	1	BD248505	ACCESSION:BD248505
c 123	7.4	37.0	10	1	CQ766664	ACCESSION:CQ766664
c 124	7.4	37.0	10	1	CQ858078	ACCESSION:CQ858078
125	7.4	37.0	10	1	CS065828	ACCESSION:CS065828
c 126	7.4	37.0	10	1	CS065828	ACCESSION:CS065828
127	7.4	37.0	10	1	CS065867	ACCESSION:CS065867
c 128	7.4	37.0	10	1	CS065867	ACCESSION:CS065867
129	7.4	37.0	10	1	DD199534	ACCESSION:DD199534
130	7.4	37.0	10	1	DD199713	ACCESSION:DD199713
c 131	7.4	37.0	10	1	E34261	ACCESSION:E34261
c 132	7.4	37.0	10	1	E39479	ACCESSION:E39479
c 133	7.4	37.0	10	1	E53843	ACCESSION:E53843
c 134	7.4	37.0	10	1	AR222953	ACCESSION:AR222953
c 135	7.4	37.0	10	1	AR282502	ACCESSION:AR282502
136	7.4	37.0	10	1	AR303309	ACCESSION:AR303309
137	7.4	37.0	10	1	AR303393	ACCESSION:AR303393
c 138	7.4	37.0	10	1	AR303484	ACCESSION:AR303484
139	7.4	37.0	10	1	AR310652	ACCESSION:AR310652
140	7.4	37.0	10	1	AR364134	ACCESSION:AR364134
c 141	7.4	37.0	10	1	AR442081	ACCESSION:AR442081
c 142	7.4	37.0	10	1	AR487048	ACCESSION:AR487048
c 143	7.4	37.0	10	1	AR585253	ACCESSION:AR585253
c 144	7.4	37.0	10	1	AR647999	ACCESSION:AR647999
145	7.4	37.0	10	1	AR696636	ACCESSION:AR696636
146	7.4	37.0	10	1	AR696640	ACCESSION:AR696640
c 147	7.4	37.0	10	1	AR778228	ACCESSION:AR778228
148	7.4	37.0	10	1	AR778232	ACCESSION:AR778232
c 149	7.4	37.0	10	1	AX021789	ACCESSION:AX021789
150	7.4	37.0	10	1	AX104930	ACCESSION:AX104930
151	7.4	37.0	10	1	AX152753	ACCESSION:AX152753
c 152	7.4	37.0	10	1	AX152924	ACCESSION:AX152924
c 153	7.4	37.0	10	1	AX153532	ACCESSION:AX153532
c 154	7.4	37.0	10	1	AX153533	ACCESSION:AX153533
c 155	7.4	37.0	10	1	AX153596	ACCESSION:AX153596
156	7.4	37.0	10	1	AX189798	ACCESSION:AX189798
157	7.4	37.0	10	1	AX189802	ACCESSION:AX189802
c 158	7.4	37.0	10	1	AX301584	ACCESSION:AX301584
c 159	7.4	37.0	10	1	AX377141	ACCESSION:AX377141
c 160	7.4	37.0	10	1	AX510724	ACCESSION:AX510724
161	7.4	37.0	10	1	AX813995	ACCESSION:AX813995
162	7.4	37.0	10	1	AX814010	ACCESSION:AX814010
c 163	6.4	32.0	10	1	AR364134	ACCESSION:AR364134

ALIGNMENTS

RESULT 1
CS097426/c
LOCUS CS097426 20 bp DNA linear PAT 03-JUN-2005
DEFINITION Sequence 69 from Patent WO2005045070.
ACCESSION CS097426
VERSION CS097426.1 GI:66953875
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lacroix,B., Krause,A., Puisieux,A. and Bachelot,T.
TITLE Method for prognosticating a breast cancer
JOURNAL Patent: WO 2005045070-A 69 19-MAY-2005;
BIOMERIEUX (FR); Centre Leon Berard (FR)
FEATURES Location/Qualifiers
source 1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 85.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGA 17
||||||||||||||||
Db 17 CCTCATGGTCACATGGA 1

RESULT 2
AR199401
LOCUS AR199401 19 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 22 from patent US 6355434.
ACCESSION AR199401
VERSION AR199401.1 GI:20249475
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Drazen,J.M., In,K.-H., Asano,K., Beier,D. and Grobholz,J.
TITLE 5-Lipoxygenase gene polymorphisms and their use in classifying patients
JOURNAL Patent: US 6355434-A 22 12-MAR-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 74.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTCATGGTCACATGGATG 19
|||||| ||| |||||||
Db 2 CTCATGCTCAGATGGATG 19

RESULT 3
AX732438/c
LOCUS AX732438 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4072 from Patent WO03025175.
ACCESSION AX732438
VERSION AX732438.1 GI:30511781
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 4072 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"

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                     /db_xref="taxon:9606"

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 10;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGAT 18
              ||| ||||| ||||||
Db         17 TCAAGGTCAAATGGAT 2


RESULT 4
CQ622872/c
LOCUS       CQ622872                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 7612 from Patent WO0192524.
ACCESSION   CQ622872
VERSION     CQ622872.1  GI:41673090
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 7612 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 14;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 5
AR463935/c
LOCUS       AR463935                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 7612 from patent US 6686188.
ACCESSION   AR463935
VERSION     AR463935.1  GI:42698992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 7612 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 14;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 6
AR180445
LOCUS       AR180445                  15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 513 from patent US 6333152.
ACCESSION   AR180445
VERSION     AR180445.1  GI:20222478
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
  TITLE     Gene expression profiles in normal and cancer cells
  JOURNAL   Patent: US 6333152-A 513 25-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 22;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              ||||| ||| ||||
Db          1 CATGGCCACGTGGA 14


RESULT 7
CQ828639/c
LOCUS       CQ828639                  11 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 357 from Patent WO2004053120.
ACCESSION   CQ828639
VERSION     CQ828639.1  GI:49732122
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1
  AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
  TITLE     Regulatory elements in the 5' region of the vr1 gene
  JOURNAL   Patent: WO 2004053120-A 357 24-JUN-2004;
            Gruenenthal GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Rattus norvegicus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10116"
                     /note="V$AP1FJ Q2"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 21;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||| |||||||
Db         11 TCAGGGTCACA 1


RESULT 8
A71522
LOCUS       A71522                    12 bp    DNA     linear   PAT 07-MAY-1999
DEFINITION  Sequence 81 from Patent WO9813521.
ACCESSION   A71522
VERSION     A71522.1  GI:4775134
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
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            unclassified sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Fesce,R. and Consalez,G.
  TITLE     METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
            PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
  JOURNAL   Patent: WO 9813521-A 81 02-APR-1998;
            FESCE RICCARDO (IT)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 26;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGG 16
              ||||||| |||
Db          2 TGGTCACGTGG 12


RESULT 9
S74610
LOCUS       S74610                   12 bp    mRNA    linear   PRI 07-MAY-1993
DEFINITION  lipoprotein lipase {exon 2-exon 3 boundary} [human, mRNA Partial
            Mutant, 12 nt].
ACCESSION   S74610
VERSION     S74610.1  GI:241423
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Gotoda,T., Yamada,N., Murase,T., Inaba,T., Ishibashi,S.,
            Shimano,H., Koga,S., Yazaki,Y., Furuichi,Y. and Takaku,F.
  TITLE     Occurrence of multiple aberrantly spliced mRNAs upon a donor splice
            site mutation that causes familial lipoprotein lipase deficiency
  JOURNAL   J. Biol. Chem. 266 (36), 24757-24762 (1991)
   PUBMED   1761570
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 74610] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1. .12
                     /gene="lipoprotein lipase, LPL"
     CDS             1. .12
                     /gene="lipoprotein lipase, LPL"
                     /note="contains in-frame 18-base pair deletion; LPL"
                     /codon_start=1
                     /product="lipoprotein lipase"
                     /protein_id="AAB20748.1"
                     /db_xref="GI:241424"
                     /translation="FMVT"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 26;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||| |||
Db          2 TCATGGTAACA 12


RESULT 10
AR759769
LOCUS       AR759769                 13 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 12 from patent US 6958240.
ACCESSION   AR759769
VERSION     AR759769.1  GI:83326505
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Baird,E.E. and Dervan,P.B.
  TITLE     Inhibition of major groove DNA binding proteins by modified
            polyamides
  JOURNAL   Patent: US 6958240-A 12 25-OCT-2005;
            California Instiute of Technology; Pasadena, CA
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 32;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db          3 TCATGGTCATA 13


RESULT 11
AR759770/c
LOCUS       AR759770                 13 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 13 from patent US 6958240.
ACCESSION   AR759770
VERSION     AR759770.1  GI:83326506
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Baird,E.E. and Dervan,P.B.
  TITLE     Inhibition of major groove DNA binding proteins by modified
            polyamides
  JOURNAL   Patent: US 6958240-A 13 25-OCT-2005;
            California Instiute of Technology; Pasadena, CA
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 32;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db         11 TCATGGTCATA 1


RESULT 12
BD124291/c
LOCUS       BD124291                 11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124291
VERSION     BD124291.1  GI:23219236
KEYWORDS    JP 2002503460-A/122.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 122 05-FEB-2002;
            THE WISTAR INSTITUTE
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COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/122
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES            Location/Qualifiers
     source         1. .11
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:10090"

  Query Match           45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGGTCACAT 14
              |||||||||
Db         10 TGGTCACAT 2


RESULT 13
AR301541/c
LOCUS       AR301541                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 122 from patent US 6538173.
ACCESSION   AR301541
VERSION     AR301541.1  GI:31689343
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 122 25-MAR-2003;
            The Wistar Institute; Philadelphia, PA;
            WOX;
FEATURES            Location/Qualifiers
     source         1. .11
                    /organism="unknown"
                    /mol_type="genomic DNA"

  Query Match           45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGGTCACAT 14
              |||||||||
Db         10 TGGTCACAT 2


RESULT 14
AX472166
LOCUS       AX472166                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 157 from Patent WO02053775.
ACCESSION   AX472166
VERSION     AX472166.1  GI:22207203
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 157 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES            Location/Qualifiers
     source         1. .11
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match           45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCACATGGA 17
              |||||||||
Db          2 TCACATGGA 10


RESULT 15
AR058623/c
LOCUS       AR058623                  12 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 200 from patent US 5837832.
ACCESSION   AR058623
VERSION     AR058623.1  GI:5984200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
            Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
  TITLE     Arrays of nucleic acid probes on biological chips
  JOURNAL   Patent: US 5837832-A 200 17-NOV-1998;
FEATURES            Location/Qualifiers
     source         1. .12
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match           45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              |||||||||
Db         11 CATGGATGA 3


RESULT 16
I04322
LOCUS       I04322                    12 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 7 from Patent EP 0147819.
ACCESSION   I04322
VERSION     I04322.1  GI:591774
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kung,H.-F. and Yamazaki,S.
  TITLE     Purification of recombinant interleukin-2
  JOURNAL   Patent: EP 0147819-A2 7 10-JUL-1985;
FEATURES            Location/Qualifiers
     source         1. .12
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match           44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 36;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              | ||||| ||||
Db          1 TTGTCACGTGGA 12
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RESULT 17
A04966
LOCUS       A04966                  10 bp    DNA     linear   PAT 28-SEP-1993
DEFINITION  Nucleotide sequence 11 from patent number EP0142268.
ACCESSION   A04966
VERSION     A04966.1  GI:488998
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Taniguchi,T., Matsui,H., Hamuro,J., Sato,T. and Sano,K.
  TITLE     Saccharomyces cerevisiae possessing gene coding for interleukin-2
            polypeptide and method for producing interleukin-2 using the yeast
  JOURNAL   Patent: EP 0142268-A 11 22-MAY-1985;
            AJINOMOTO CO., INC.; JAPANESE FOUNDATION FOR CANCER RESEARCH
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              || |||||||
Db          1 ACGTGGATGA 10


RESULT 18
BD166495/c
LOCUS       BD166495                10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166495
VERSION     BD166495.1  GI:27872307
KEYWORDS    JP 2002209591-A/40.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 40 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/40
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db         10 CTCTTGGTCA 1


RESULT 19
BD167034/c
LOCUS       BD167034                10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167034
VERSION     BD167034.1  GI:27872846
KEYWORDS    JP 2002209591-A/579.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 579 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/579
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db         10 CTCTTGGTCA 1


RESULT 20
CQ858077/c
LOCUS       CQ858077                10 bp    DNA     linear   PAT 31-AUG-2004
DEFINITION  Sequence 136 from Patent WO2004069189.
ACCESSION   CQ858077
VERSION     CQ858077.1  GI:51852182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Branch,R.A. and Romkes,M.
  TITLE     Methods of assessment of drug metabolizing enzymes
  JOURNAL   Patent: WO 2004069189-A 136 19-AUG-2004;
            Innovaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Synthetic
                     oligonucleotide"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          5 ATGGTCACAT 14
              ||||||||| |
Db         10 ATGGTCACCT 1


RESULT 21
AR194807
LOCUS       AR194807                  10 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 29 from patent US 6350447.
ACCESSION   AR194807
VERSION     AR194807.1  GI:20244244
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.Paul. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6350447-A 29 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 ACATGGATGA 20
               ||| ||||||
Db           1 ACAAGGATGA 10


RESULT 22
I54941
LOCUS       I54941                    10 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 31 from patent US 5646126.
ACCESSION   I54941
VERSION     I54941.1  GI:2476144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Cheng,Y.-c., Lukhtanov,E.A., Meyer,R.B. Jr., Pai,B.S., Reed,M.W.
            and Zhou,J.H.
  TITLE     Sterol modified oligonucleotide duplexes having anticancer activity
  JOURNAL   Patent: US 5646126-A 31 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          10 CACATGGATG 19
               ||||||| ||
Db           1 CACATGGGTG 10


RESULT 23
I54945
LOCUS       I54945                    10 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 35 from patent US 5646126.
ACCESSION   I54945
VERSION     I54945.1  GI:2476148
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Cheng,Y.-c., Lukhtanov,E.A., Meyer,R.B. Jr., Pai,B.S., Reed,M.W.
            and Zhou,J.H.
  TITLE     Sterol modified oligonucleotide duplexes having anticancer activity
  JOURNAL   Patent: US 5646126-A 35 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          10 CACATGGATG 19
               |||| |||||
Db           1 CACACGGATG 10


RESULT 24
AR562123
LOCUS       AR562123                  10 bp    RNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 29 from patent US 6759214.
ACCESSION   AR562123
VERSION     AR562123.1  GI:53975973
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6759214-A 29 06-JUL-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 ACATGGATGA 20
               ||| ||||||
Db           1 ACAAGGATGA 10


RESULT 25
AR567221
LOCUS       AR567221                  10 bp    RNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 29 from patent US 6780410.
ACCESSION   AR567221
VERSION     AR567221.1  GI:53984870
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6780410-A 29 24-AUG-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          11 ACATGGATGA 20
               ||| ||||||
Db           1 ACAAGGATGA 10


RESULT 26
AR567927
LOCUS       AR567927                  10 bp    RNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 29 from patent US 6780977.
ACCESSION   AR567927
VERSION     AR567927.1  GI:53986145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6780977-A 29 24-AUG-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 ACATGGATGA 20
               ||| ||||||
Db           1 ACAAGGATGA 10


RESULT 27
AR577802
LOCUS       AR577802                  10 bp    RNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 29 from patent US 6783959.
ACCESSION   AR577802
VERSION     AR577802.1  GI:56580558
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6783959-A 29 31-AUG-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 ACATGGATGA 20
               ||| ||||||
Db           1 ACAAGGATGA 10


RESULT 28
AR580135
LOCUS       AR580135                  10 bp    RNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6787328.
ACCESSION   AR580135
VERSION     AR580135.1  GI:56610137
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6787328-A 29 07-SEP-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 ACATGGATGA 20
               ||| ||||||
Db           1 ACAAGGATGA 10


RESULT 29
AR614595
LOCUS       AR614595                  10 bp    RNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6828423.
ACCESSION   AR614595
VERSION     AR614595.1  GI:56670943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6828423-A 29 07-DEC-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 ACATGGATGA 20
               ||| ||||||
Db           1 ACAAGGATGA 10


RESULT 30
AR652778
LOCUS       AR652778                  10 bp    RNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 29 from patent US 6884872.
ACCESSION   AR652778
VERSION     AR652778.1  GI:67580837
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6884872-A 29 26-APR-2005;
            NUVELO, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"
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  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| ||||||
Db          1 ACAAGGATGA 10


RESULT 31
AR659094
LOCUS       AR659094                  10 bp    RNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 29 from patent US 6899875.
ACCESSION   AR659094
VERSION     AR659094.1  GI:67594994
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chadwick,B.P. and Frischauf,A.-M.
  TITLE     Methods and compositions relating to CD39-like polypeptides and
            nucleic acids
  JOURNAL   Patent: US 6899875-A 29 31-MAY-2005;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              ||| ||||||
Db          1 ACAAGGATGA 10


RESULT 32
AX152149
LOCUS       AX152149                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 64 from Patent WO0138577.
ACCESSION   AX152149
VERSION     AX152149.1  GI:14533800
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 64 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 TCACATGGAT 18
              |||||| |||
Db          1 TCACATTGAT 10


RESULT 33
CQ835676
LOCUS       CQ835676                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 734 from Patent WO2004059001.
ACCESSION   CQ835676
VERSION     CQ835676.1  GI:50835210
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 734 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db          2 ATATGGATGA 11


RESULT 34
CQ835701/c
LOCUS       CQ835701                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 759 from Patent WO2004059001.
ACCESSION   CQ835701
VERSION     CQ835701.1  GI:50835235
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 759 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              || |||||||
Db         10 CAGATGGATG 1


RESULT 35
CQ835852/c
LOCUS       CQ835852                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 910 from Patent WO2004059001.
ACCESSION   CQ835852
VERSION     CQ835852.1  GI:50835386
KEYWORDS    .
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 910 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACAT 14
              |||||| |||
Db         11 ATGGTCCCAT 2


RESULT 36
AX470966
LOCUS       AX470966                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 543 from Patent WO02053773.
ACCESSION   AX470966
VERSION     AX470966.1  GI:22206091
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 543 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db          2 CTCGTGGTCA 11


RESULT 37
AX624145
LOCUS       AX624145                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1186 from Patent WO02053774.
ACCESSION   AX624145
VERSION     AX624145.1  GI:28452086
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1186 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db          2 CTCGTGGTCA 11


RESULT 38
AX625704/c
LOCUS       AX625704                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2745 from Patent WO02053774.
ACCESSION   AX625704
VERSION     AX625704.1  GI:28453645
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2745 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 TCACATGGAT 18
              ||||| ||||
Db         10 TCACAGGGAT 1


RESULT 39
AX626419/c
LOCUS       AX626419                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3460 from Patent WO02053774.
ACCESSION   AX626419
VERSION     AX626419.1  GI:28454457
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3460 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
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  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACAT 14
              |||||| |||
Db         11 ATGGTCCCAT 2


RESULT 40
AX631566
LOCUS       AX631566                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8608 from Patent WO02053774.
ACCESSION   AX631566
VERSION     AX631566.1  GI:28459642
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8608 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              ||| ||||||
Db          2 CTCGTGGTCA 11


RESULT 41
AR024074/c
LOCUS       AR024074                  12 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 24 from patent US 5795778.
ACCESSION   AR024074
VERSION     AR024074.1  GI:3977368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 5795778-A 24 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 42
AR075457/c
LOCUS       AR075457                  12 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 10 from patent US 5958424.
ACCESSION   AR075457
VERSION     AR075457.1  GI:10002207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and De Boer,G.F.
  TITLE     Recombinant chicken anemia virus particle
  JOURNAL   Patent: US 5958424-A 10 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 43
AR108947/c
LOCUS       AR108947                  12 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6113913.
ACCESSION   AR108947
VERSION     AR108947.1  GI:12825223
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brough,D.E. and Kovesdi,I.
  TITLE     Recombinant adenovirus
  JOURNAL   Patent: US 6113913-A 2 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 44
AR153908/c
LOCUS       AR153908                  12 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 10 from patent US 6238669.
ACCESSION   AR153908
VERSION     AR153908.1  GI:15121961
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and De Boer,G.F.
  TITLE     Proteins encoded by chicken anemia virus DNA and diagnostic kits
            and vaccines employing said proteins
  JOURNAL   Patent: US 6238669-A 10 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 45
AR172244/c
LOCUS       AR172244                  12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 68 from patent US 6303295.
ACCESSION   AR172244
VERSION     AR172244.1  GI:17911735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Taylor,E.Will., Nadimpalli,R.Gopal. and Ramanathan,C.Sekar.
  TITLE     Selenoproteins, coding sequences and methods
  JOURNAL   Patent: US 6303295-A 68 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         11 CTCAGGGTCA 2


RESULT 46
AR178525/c
LOCUS       AR178525                  12 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 10 from patent US 6319693.
ACCESSION   AR178525
VERSION     AR178525.1  GI:20219663
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and de Boer,G.F.
  TITLE     Cloning of chicken anemia virus DNA
  JOURNAL   Patent: US 6319693-A 10 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 47
BD001178/c
LOCUS       BD001178                  12 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001178
VERSION     BD001178.1  GI:18625737
KEYWORDS    JP 2000342285-A/338.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G.; Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342285-A 338 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342285-A/338
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132616
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 48
BD001607/c
LOCUS       BD001607                  12 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001607
VERSION     BD001607.1  GI:18626166
KEYWORDS    JP 2000342286-A/338.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342286-A 338 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342286-A/338
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132651
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
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          14-MAY-1992 US     07/884074,14-MAY-1992 US     07/884333 PR
          14-MAY-1992 US     07/884422,14-MAY-1992 US     07/884431 PR
          14-MAY-1992 US     07/884436,14-MAY-1992 US     07/884521 PR
          31-JUL-1992 US     07/923738,26-AUG-1992 US     07/935854 PR
          26-AUG-1992 US     07/936086,18-SEP-1992 US     07/948359 PR
          15-OCT-1992 US     07/963322,07-DEC-1992 US     07/987129 PR
          07-DEC-1992 US     07/987130,07-DEC-1992 US     07/987133 PI
          KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
          MAYSEJAK,
          PI   JAMES J HOLESEK,ANTHONY J MAMONE
          PC   C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
          PC   A61K39/135,
          PC   A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
          PC   A61P1/16,
          PC   A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
            (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
            C12R1:93)
          CC
          FH   Key             Location/Qualifiers
          FT   source          1. .12
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 49
BD064941/c
LOCUS       BD064941                12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA.
ACCESSION   BD064941
VERSION     BD064941.1  GI:22610544
KEYWORDS    JP 2001275678-A/153.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and
            Nishikawa,K.
  TITLE     Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA
  JOURNAL   Patent: JP 2001275678-A 153 09-OCT-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001275678-A/153
            PD   09-OCT-2001
            PF   31-MAR-2000 JP 2000096306
            PI   TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI
            MIMAKI,REI FUKUSHIMA,
            PI   KAZUKO NISHIKAWA
            PC   C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC
            Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 50
BD240723/c
LOCUS       BD240723                12 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Replication-deficient recombinant adenovirus having mutation major
            late promoter.
ACCESSION   BD240723
VERSION     BD240723.1  GI:33050493
KEYWORDS    JP 2002519036-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brough,D.E. and Kovesdi,I.
  TITLE     Replication-deficient recombinant adenovirus having mutation major
            late promoter
  JOURNAL   Patent: JP 2002519036-A 2 02-JUL-2002;
            GENVEC INC
COMMENT     OS   Human adenovirus serotype 5
            PN   JP 2002519036-A/2
            PD   02-JUL-2002
            PF   24-JUN-1999 JP 2000557381
            PR   26-JUN-1998 US    09/105515
            PI   DOUGLAS E BROUGH,IMRE KOVESDI
            PC   C12N15/09,C12N5/10,C12N7/00//A61K35/76,A61K39/235,A61K48/00,
            PC   C12N15/00,
            PC   C12N5/00
            CC   Replication-deficient recombinant adenovirus having mutation
            CC            major late
            CC   promoter
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Human adenovirus serotype 5'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 51
BD261806
LOCUS       BD261806                12 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Enhancement in protein production by higher plants using ubiquitin
            or cucumber mosaic virus coating protein peptide.
ACCESSION   BD261806
VERSION     BD261806.1  GI:33071574
KEYWORDS    JP 2002532098-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Fang,R.X., Wu,J.L. and Chen,X.Y.
  TITLE     Enhancement in protein production by higher plants using ubiquitin
            or cucumber mosaic virus coating protein peptide
  JOURNAL   Patent: JP 2002532098-A 10 02-OCT-2002;
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            INSTITUTE OF MOLECULAR AGROBIOLOGY
COMMENT     OS   Plasmid pCL
            PN   JP 2002532098-A/10
            PD   02-OCT-2002
            PF   11-DEC-1998 JP 2000588378
            PI   RONG XIANG FANG,JUNG LIN WU,XIAO YING CHEN
            PC   C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC
              C12N5/00
            CC   Joining region between fusion of genes.
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(12).
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGA 17
              ||| ||||||
Db          2 GTCGCATGGA 11


RESULT 52
CQ828540
LOCUS       CQ828540                  12 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 258 from Patent WO2004053120.
ACCESSION   CQ828540
VERSION     CQ828540.1  GI:49732023
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1
  AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
  TITLE     Regulatory elements in the 5' region of the vr1 gene
  JOURNAL   Patent: WO 2004053120-A 258 24-JUN-2004;
            Gruenenthal GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="Rattus norvegicus"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:10116"
                      /note="V$IK2 01"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              |||| |||||
Db          1 CACAGGGATG 10


RESULT 53
I17542/c
LOCUS       I17542                    12 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 10 from patent US 5491073.
ACCESSION   I17542
VERSION     I17542.1  GI:1597897
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and de Boer,G.F.
  TITLE     Cloning of chicken anaemia DNA
  JOURNAL   Patent: US 5491073-A 10 13-FEB-1996;
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 54
AR224293/c
LOCUS       AR224293                  12 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 24 from patent US 6440719.
ACCESSION   AR224293
VERSION     AR224293.1  GI:23333070
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 6440719-A 24 27-AUG-2002;
            Ribozyme Pharmaceuticals, Inc.; Boulder, CO
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 55
AR234464/c
LOCUS       AR234464                  12 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6458578.
ACCESSION   AR234464
VERSION     AR234464.1  GI:27277166
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brough,D.E. and Kovesdi,I.
  TITLE     Recombinant cell line produces adenoviral gene products E1 and
            DEF-A, and/or DEF-B
  JOURNAL   Patent: US 6458578-A 2 01-OCT-2002;
            GenVec, Inc.; Gaithersburg, MD
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3
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RESULT 56
AR275829/c
LOCUS       AR275829                  12 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 10 from patent US 6509446.
ACCESSION   AR275829
VERSION     AR275829.1  GI:29709474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and De Boer,G.F.
  TITLE     Cloning of chicken anemia DNA
  JOURNAL   Patent: US 6509446-A 10 21-JAN-2003;
            Leadd B.V.; Leiden;
            NLX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              ||||||  |||
Db         12 GGTCACGTGG 3


RESULT 57
I58612/c
LOCUS       I58612                    12 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5652144.
ACCESSION   I58612
VERSION     I58612.1  GI:2477850
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Lu,Y. and Haseltine,W.A.
  TITLE     YC1 gene
  JOURNAL   Patent: US 5652144-A 3 29-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              ||||||  |||
Db         12 GGTCACGTGG 3


RESULT 58
I72395/c
LOCUS       I72395                    12 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 26 from patent US 5683985.
ACCESSION   I72395
VERSION     I72395.1  GI:3008534
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Chu,B.Chen.Fei. and Orgel,L.
  TITLE     Oligonucleotide decoys and methods relating thereto
  JOURNAL   Patent: US 5683985-A 26 04-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              ||||||  |||
Db         12 GGTCACGTGG 3


RESULT 59
AR577337
LOCUS       AR577337                  12 bp    DNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 54 from patent US 6777544.
ACCESSION   AR577337
VERSION     AR577337.1  GI:56579871
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E., Breipohl,G. and Will,D.W.
  TITLE     Polyamide nucleic acid derivatives and agents and processes for
            preparing them
  JOURNAL   Patent: US 6777544-A 54 17-AUG-2004;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 60
AR699868
LOCUS       AR699868                  12 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 38 from patent US 6919441.
ACCESSION   AR699868
VERSION     AR699868.1  GI:75205772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E. and Breipohl,G.
  TITLE     Polyamide-oligonucleotide derivatives, their preparation and use
  JOURNAL   Patent: US 6919441-A 38 19-JUL-2005;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11
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RESULT 61
AR699877
LOCUS       AR699877                  12 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 48 from patent US 6919441.
ACCESSION   AR699877
VERSION     AR699877.1  GI:75205785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E. and Breipohl,G.
  TITLE     Polyamide-oligonucleotide derivatives, their preparation and use
  JOURNAL   Patent: US 6919441-A 48 19-JUL-2005;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 62
AR699878/c
LOCUS       AR699878                  12 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 49 from patent US 6919441.
ACCESSION   AR699878
VERSION     AR699878.1  GI:75205786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E. and Breipohl,G.
  TITLE     Polyamide-oligonucleotide derivatives, their preparation and use
  JOURNAL   Patent: US 6919441-A 49 19-JUL-2005;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db         11 CATCATGGTC 2


RESULT 63
AX283286
LOCUS       AX283286                  12 bp    DNA     linear   PAT 20-NOV-2001
DEFINITION  Sequence 50 from Patent WO0179249.
ACCESSION   AX283286
VERSION     AX283286.1  GI:17044167
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Uhlmann,E., Breipohl,G. and Will,D.W.
  TITLE     Polyamide nucleic acid derivatives, agents and methods for
            producing the same
  JOURNAL   Patent: WO 0179249-A 50 25-OCT-2001;
            Aventis Pharma Deutschland GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen Sequenz:
                     Oligonukleotide"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 64
AX711060/c
LOCUS       AX711060                  12 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 360 from Patent EP1288296.
ACCESSION   AX711060
VERSION     AX711060.1  GI:29787441
KEYWORDS    .
SOURCE      Herpes simplex virus unknown type
  ORGANISM  Herpes simplex virus unknown type
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Alphaherpesvirinae; Simplexvirus; unclassified Simplexvirus.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 360 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Herpes simplex virus unknown type"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:126283"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 65
A41398
LOCUS       A41398                    10 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 24 from Patent WO9426928.
ACCESSION   A41398
VERSION     A41398.1  GI:2297117
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Strauss,M. and Bauer,D.
  TITLE     COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
            DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT
  JOURNAL   Patent: WO 9426928-A 24 24-NOV-1994;
            MAX PLANCK GESELLSCHAFT (DE)
COMMENT     Other publication DE 4317414 940421.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 66
AR030211/c
LOCUS       AR030211                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 22 from patent US 5861246.
ACCESSION   AR030211
VERSION     AR030211.1  GI:5943425
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Weissman,S.M., Nallur,G.N. and Kulkarni,P.
  TITLE     Multiple selection process for binding sites of DNA-binding
            proteins
  JOURNAL   Patent: US 5861246-A 22 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              ||||||||
Db         10 CATGGATG 3


RESULT 67
BD083377
LOCUS       BD083377                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human matured/activated dendritic cell expression genes.
ACCESSION   BD083377
VERSION     BD083377.1  GI:22628987
KEYWORDS    JP 2001327293-A/298.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
  TITLE     Human matured/activated dendritic cell expression genes
  JOURNAL   Patent: JP 2001327293-A 298 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001327293-A/298
            PD   27-NOV-2001
            PF   22-MAY-2000 JP 2000150562
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
              NAGAI
            PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           2 ATGGATGA 9


RESULT 68
BD238706
LOCUS       BD238706                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238706
VERSION     BD238706.1  GI:33048476
KEYWORDS    JP 2002534056-A/124.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 124 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/124
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ATGGATGA 20
               ||||||||
Db           2 ATGGATGA 9


RESULT 69
BD240099
LOCUS       BD240099                  10 bp    DNA     linear   PAT 17-JUL-2003
```

```
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240099
VERSION     BD240099.1  GI:33049869
KEYWORDS    JP 2002534056-A/1517.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1517 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1517
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACAT 14
              ||||||||
Db          1 GGTCACAT 8


RESULT 70
I22203
LOCUS       I22203                    10 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 17 from patent US 5527671.
ACCESSION   I22203
VERSION     I22203.1  GI:1602557
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Li,K., Rouse,D.I. and German,T.L.
  TITLE     Assay for verticillium dahliae
  JOURNAL   Patent: US 5527671-A 17 18-JUN-1996;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          1 ATGGATGA 8


RESULT 71
AR303481
LOCUS       AR303481                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 206 from patent US 6544736.
ACCESSION   AR303481
VERSION     AR303481.1  GI:31692257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 206 08-APR-2003;
            Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.;
            Tokyo;
            JPX;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTC 10
              ||||||||
Db          3 TCATGGTC 10


RESULT 72
BD106575
LOCUS       BD106575                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Production of attenuated parainfluenza virus vaccines from cloned
            nucleotide sequence.
ACCESSION   BD106575
VERSION     BD106575.1  GI:23201393
KEYWORDS    JP 2002502241-A/69.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Murphy,B.R., Collins,P.L., Durbin,A.P., Skiadopoulos,M.H. and Ta,T.
  TITLE     Production of attenuated parainfluenza virus vaccines from cloned
            nucleotide sequence
  JOURNAL   Patent: JP 2002502241-A 69 22-JAN-2002;
            THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
            THE MERCK & CO INC DEPARTMENT OF HEALTH AND HUMANSERVICES
COMMENT     PN   JP 2002502241-A/69
            PD   22-JAN-2002
            PF   22-MAY-1998 JP 1998550704
            PR   23-MAY-1997 US    60/047575,19-SEP-1997 US    60/059385 PI
            BRIAN R MURPHY,PETER L COLLINS,ANNA P DURBIN,MARIO H  PI
            SKIADOPOULOS,TAO TAO
            PC   C12N15/45,C07K14/115,C12N5/10,C12N7/01,A61K39/155 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
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FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCACATGG 16
              ||||||||
Db          1 TCACATGG 8


RESULT 73
CQ828725/c
LOCUS       CQ828725                  11 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 443 from Patent WO2004053120.
ACCESSION   CQ828725
VERSION     CQ828725.1  GI:49732208
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
  TITLE     Regulatory elements in the 5' region of the vr1 gene
  JOURNAL   Patent: WO 2004053120-A 443 24-JUN-2004;
            Gruenenthal GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"
                     /note="V$AP1FJ Q2"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 ATGGTCAC 12
              ||||||||
Db          9 ATGGTCAC 2


RESULT 74
CS058623
LOCUS       CS058623                  11 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 520 from Patent WO2005028671.
ACCESSION   CS058623
VERSION     CS058623.1  GI:62551806
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
  TITLE     Method for determining hair cycle markers
  JOURNAL   Patent: WO 2005028671-A 520 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 75
AR636603
LOCUS       AR636603                  11 bp    RNA     linear   PAT 20-APR-2005
DEFINITION  Sequence 20 from patent US 6855498.
ACCESSION   AR636603
VERSION     AR636603.1  GI:62769610
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Hester,J.D., Lindquist,H.D.A. and Schaefer,F.W. III.
  TITLE     In-situ hybridization probes for the detection of microsporidial
            species
  JOURNAL   Patent: US 6855498-A 20 15-FEB-2005;
            U.S. Environmental Protection Agency; Washington, DC
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCACATGG 16
              ||||||||
Db          3 TCACATGG 10


RESULT 76
AX471749
LOCUS       AX471749                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1326 from Patent WO02053773.
ACCESSION   AX471749
VERSION     AX471749.1  GI:22206874
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1326 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 77
AX472076/c
LOCUS       AX472076                  11 bp    DNA     linear   PAT 09-AUG-2002
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```
DEFINITION  Sequence 67 from Patent WO02053775.
ACCESSION   AX472076
VERSION     AX472076.1  GI:22207117
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 67 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 ACATGGAT 18
               ||||||||
Db           8 ACATGGAT 1


RESULT 78
AX472088
LOCUS       AX472088                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 79 from Patent WO02053775.
ACCESSION   AX472088
VERSION     AX472088.1  GI:22207129
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 79 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 CACATGGA 17
               ||||||||
Db           4 CACATGGA 11


RESULT 79
AX628092/c
LOCUS       AX628092                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5133 from Patent WO02053774.
ACCESSION   AX628092
VERSION     AX628092.1  GI:28456130
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5133 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           6 TGGTCACA 13
               ||||||||
Db          11 TGGTCACA 4


RESULT 80
BD124230
LOCUS       BD124230                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124230
VERSION     BD124230.1  GI:23219175
KEYWORDS    JP 2002503460-A/61.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 61 05-FEB-2002;
            THE WISTAR INSTITUTE
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/61
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           2 CTCATGGTCAC 12
               ||| ||| |||
Db           1 CTCCTGGACAC 11


RESULT 81
BD124372
LOCUS       BD124372                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124372
VERSION     BD124372.1  GI:23219317
```

```
KEYWORDS    JP 2002503460-A/203.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 203 05-FEB-2002;
            THE WISTAR INSTITUTE
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/203
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:10090"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||| ||| |||
Db          1 CTCCTGGACAC 11


RESULT 82
CQ832782/c
LOCUS       CQ832782                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 153 from Patent WO2004059002.
ACCESSION   CQ832782
VERSION     CQ832782.1  GI:50832389
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining the homeostasis of hairy skin
  JOURNAL   Patent: WO 2004059002-A 153 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              |||  |||||
Db         11 TCAGTGTCACA 1


RESULT 83
CQ832880
LOCUS       CQ832880                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 251 from Patent WO2004059002.
ACCESSION   CQ832880
VERSION     CQ832880.1  GI:50832487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining the homeostasis of hairy skin
  JOURNAL   Patent: WO 2004059002-A 251 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              ||| || ||||
Db          1 CATCGTTACAT 11


RESULT 84
CQ833337/c
LOCUS       CQ833337                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 708 from Patent WO2004059002.
ACCESSION   CQ833337
VERSION     CQ833337.1  GI:50832944
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining the homeostasis of hairy skin
  JOURNAL   Patent: WO 2004059002-A 708 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||  |||| |||
Db         11 TCTTGGTAACA 1


RESULT 85
CQ837472
LOCUS       CQ837472                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 2530 from Patent WO2004059001.
ACCESSION   CQ837472
VERSION     CQ837472.1  GI:50837006
KEYWORDS    .
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 2530 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATG 15
              |||||| | ||
Db          1 ATGGTCTCCTG 11


RESULT 86
CS058638/c
LOCUS       CS058638                  11 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 535 from Patent WO2005028671.
ACCESSION   CS058638
VERSION     CS058638.1  GI:62551821
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
  TITLE     Method for determining hair cycle markers
  JOURNAL   Patent: WO 2005028671-A 535 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              | | |||||||
Db         11 CCCGTGGTCAC 1


RESULT 87
AR301480
LOCUS       AR301480                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 61 from patent US 6538173.
ACCESSION   AR301480
VERSION     AR301480.1  GI:31689282
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 61 25-MAR-2003;
            The Wistar Institute; Philadelphia, PA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||| ||| |||
Db          1 CTCCTGGACAC 11


RESULT 88
AR301622
LOCUS       AR301622                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 203 from patent US 6538173.
ACCESSION   AR301622
VERSION     AR301622.1  GI:31689424
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 203 25-MAR-2003;
            The Wistar Institute; Philadelphia, PA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||| ||| |||
Db          1 CTCCTGGACAC 11


RESULT 89
AR305523/c
LOCUS       AR305523                  11 bp    RNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 54 from patent US 6545140.
ACCESSION   AR305523
VERSION     AR305523.1  GI:31694891
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Harmon,B.G., Jackwood,M.W. and Brockus,C.W.
  TITLE     DNA encoding an avian beta-defensin and uses thereof
  JOURNAL   Patent: US 6545140-A 54 08-APR-2003;
            University of Georgia Research Foundation, Inc.; Athens, GA
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match           39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              ||||||  |||
Db         11 CATGGTTTCAT 1
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RESULT 90
I54914
LOCUS       I54914                    11 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 4 from patent US 5646126.
ACCESSION   I54914
VERSION     I54914.1  GI:2476117
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Cheng,Y.-c., Lukhtanov,E.A., Meyer,R.B. Jr., Pai,B.S., Reed,M.W.
            and Zhou,J.H.
  TITLE     Sterol modified oligonucleotide duplexes having anticancer activity
  JOURNAL   Patent: US 5646126-A 4 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CACATGGATGA 20
              |||| || |||
Db          1 CACACGGGTGA 11


RESULT 91
AR488869
LOCUS       AR488869                  11 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 98 from patent US 6709817.
ACCESSION   AR488869
VERSION     AR488869.1  GI:47255067
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zoghbi,H.Y., Van den Veyver,I.B., Amir,R. and Francke,U.
  TITLE     Method of screening Rett syndrome by detecting a mutation in MECP2
  JOURNAL   Patent: US 6709817-A 98 23-MAR-2004;
            Baylor College of Medicine; Houston, TX
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCA 11
              | ||||||| |
Db          1 CTTCATGGTAA 11


RESULT 92
AX623060
LOCUS       AX623060                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 101 from Patent WO02053774.
ACCESSION   AX623060
VERSION     AX623060.1  GI:28451001
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 101 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CACATGGATGA 20
              |||| ||| ||
Db          1 CACAGGGAGGA 11


RESULT 93
AX624268
LOCUS       AX624268                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1309 from Patent WO02053774.
ACCESSION   AX624268
VERSION     AX624268.1  GI:28452209
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1309 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 TCACATGGATG 19
              ||||| || ||
Db          1 TCACAAGGCTG 11


RESULT 94
AX625114
LOCUS       AX625114                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2155 from Patent WO02053774.
ACCESSION   AX625114
VERSION     AX625114.1  GI:28453055
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2155 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              ||| || ||||
Db          1 CATCGTTACAT 11


RESULT 95
AX626525/c
LOCUS       AX626525                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3566 from Patent WO02053774.
ACCESSION   AX626525
VERSION     AX626525.1  GI:28454563
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3566 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGG 16
              || ||| ||||
Db         11 TGATCATATGG 1


RESULT 96
AX626963
LOCUS       AX626963                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4004 from Patent WO02053774.
ACCESSION   AX626963
VERSION     AX626963.1  GI:28455001
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4004 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACAT 14
              |||  ||||||
Db          1 CATATTCACAT 11


RESULT 97
AX627369
LOCUS       AX627369                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4410 from Patent WO02053774.
ACCESSION   AX627369
VERSION     AX627369.1  GI:28455407
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4410 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCA 11
              || | ||||||
Db          1 CCCCGTGGTCA 11


RESULT 98
AX627724
LOCUS       AX627724                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4765 from Patent WO02053774.
ACCESSION   AX627724
VERSION     AX627724.1  GI:28455762
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4765 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATG 15
              |||||| | ||
Db          1 ATGGTCTCCTG 11


RESULT 99
AX627923/c
LOCUS       AX627923                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4964 from Patent WO02053774.
ACCESSION   AX627923
VERSION     AX627923.1  GI:28455961
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4964 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              |||  ||||||
Db         11 TCAGTGTCACA 1


RESULT 100
AX628352
LOCUS       AX628352                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5393 from Patent WO02053774.
ACCESSION   AX628352
VERSION     AX628352.1  GI:28456390
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5393 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              || ||||||  |
Db          1 CTTATGGTCCC 11


RESULT 101
AX630481
LOCUS       AX630481                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7522 from Patent WO02053774.
ACCESSION   AX630481
VERSION     AX630481.1  GI:28458519
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7522 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CACATGGATGA 20
              |||| ||| ||
Db          1 CACAGGGAGGA 11


RESULT 102
AX631689
LOCUS       AX631689                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8731 from Patent WO02053774.
ACCESSION   AX631689
VERSION     AX631689.1  GI:28459796
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8731 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 TCACATGGATG 19
              ||||| || ||
Db          1 TCACAAGGCTG 11


RESULT 103
AX632535
LOCUS       AX632535                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9577 from Patent WO02053774.
ACCESSION   AX632535
VERSION     AX632535.1  GI:28468150
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9577 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 49;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          4 CATGGTCACAT 14
              ||| || ||||
Db          1 CATCGTTACAT 11


RESULT 104
AX669046/c
LOCUS       AX669046                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2495 from Patent WO0242459.
ACCESSION   AX669046
VERSION     AX669046.1  GI:29292023
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2495 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGG 16
              |||||| ||
Db          9 GTCACACGG 1


RESULT 105
AX669047/c
LOCUS       AX669047                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2496 from Patent WO0242459.
ACCESSION   AX669047
VERSION     AX669047.1  GI:29292024
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2496 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGG 16
              |||||| ||
Db          9 GTCACACGG 1


RESULT 106
AR004936/c
LOCUS       AR004936                 10 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5747299.
ACCESSION   AR004936
VERSION     AR004936.1  GI:3965815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Bloom,D., Fathman,C.Garrison. and Slaymaker,S.
  TITLE     Anergy genes
  JOURNAL   Patent: US 5747299-A 3 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 107
AR036563/c
LOCUS       AR036563                 10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5872235.
ACCESSION   AR036563
VERSION     AR036563.1  GI:5953231
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chen,L.Bo., Bao,S. and Liu,Y.
  TITLE     Nucleic acids encoding tumor marker
  JOURNAL   Patent: US 5872235-A 16 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 108
BD007825/c
LOCUS       BD007825                 10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007825
VERSION     BD007825.1  GI:18636198
KEYWORDS    JP 2001069993-A/101.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 101 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/101
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
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            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATG 15
              ||||||| |
Db          9 GGTCACACG 1


RESULT 109
BD065345/c
LOCUS       BD065345                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065345
VERSION     BD065345.1  GI:22610948
KEYWORDS    JP 2001509017-A/281.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 281 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/281
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
            C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Saccharomyces cerevisiae"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:4932"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              ||| |||||
Db         10 CATCGTCAC 2


RESULT 110
BD091128/c
LOCUS       BD091128                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  P53-induced apoptosis.
ACCESSION   BD091128
VERSION     BD091128.1  GI:22636738
KEYWORDS    JP 2001523441-A/6.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Vogelstein,B., Kinzler,K.W. and Polyak,K.
  TITLE     P53-induced apoptosis
  JOURNAL   Patent: JP 2001523441-A 6 27-NOV-2001;
            THE JOHNS HOPKINS UNIVERSITY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001523441-A/6
            PD   27-NOV-2001
            PF   17-SEP-1998 JP 2000511894
            PR   17-SEP-1997 US    60/059153,30-MAR-1998 US    60/079817 PI
            BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
            C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC   P53-induced
            apoptosis
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 111
BD161260/c
LOCUS       BD161260                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161260
VERSION     BD161260.1  GI:27867018
KEYWORDS    JP 2002186482-A/82.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 82 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/82
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 112
BD161382/c
LOCUS       BD161382                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161382
VERSION     BD161382.1  GI:27867140
KEYWORDS    JP 2002186482-A/204.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 204 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/204
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              ||| |||||
Db          9 CTCCTGGTC 1


RESULT 113
BD166523/c
LOCUS       BD166523                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166523
VERSION     BD166523.1  GI:27872335
KEYWORDS    JP 2002209591-A/68.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 68 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/68
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 114
BD166590/c
LOCUS       BD166590                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166590
VERSION     BD166590.1  GI:27872402
KEYWORDS    JP 2002209591-A/135.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 135 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/135
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              || ||||||
Db          9 CAGGGTCAC 1


RESULT 115
BD166762/c
LOCUS       BD166762                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166762
VERSION     BD166762.1  GI:27872574
KEYWORDS    JP 2002209591-A/307.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
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  JOURNAL   Patent: JP 2002209591-A 307 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/307
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              || ||||||
Db          9 CAGGGTCAC 1


RESULT 116
BD167122/c
LOCUS       BD167122                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167122
VERSION     BD167122.1  GI:27872934
KEYWORDS    JP 2002209591-A/667.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 667 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/667
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 117
BD167240/c
LOCUS       BD167240                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167240
VERSION     BD167240.1  GI:27873052
KEYWORDS    JP 2002209591-A/785.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 785 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/785
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 118
BD167877/c
LOCUS       BD167877                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  PCA2501 gene.
ACCESSION   BD167877
VERSION     BD167877.1  GI:27873689
KEYWORDS    WO 0238763-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Asaoka,H., Kaneda,K., Adachi,M. and Miyanaga,K.
  TITLE     PCA2501 gene
  JOURNAL   Patent: WO 0238763-A 3 16-MAY-2002;
            JAPAN IMMUNORESEARCH LABORATORIES CO LTD,HIDEYUKI ASAOKA, KENTA
            KANEDA, MASAKAZU ADACHI,KAZUO MIYANAGA
COMMENT     OS   Artificial Sequence
            PN   WO 0238763-A/3
            PD   16-MAY-2002
            PF   31-OCT-2001 WO 2001JP009545
            PR   09-NOV-2000 JP 00P   341998
            PI   HIDEYUKI ASAOKA,KENTA KANEDA,MASAKAZU ADACHI,KAZUO MIYANAGA PC
              C12N15/12,C12Q1/68,A61K48/00
            CC   PCA2501 gene
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 119
BD238612/c
LOCUS       BD238612                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238612
VERSION     BD238612.1  GI:33048382
KEYWORDS    JP 2002534056-A/30.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 30 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/30
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           4 CATGGTCAC 12
               | |||||||
Db           9 CGTGGTCAC 1


RESULT 120
BD239861/c
LOCUS       BD239861                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239861
VERSION     BD239861.1  GI:33049631
KEYWORDS    JP 2002534056-A/1279.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1279 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1279
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 GGTCACATG 15
               ||||||| |
Db          10 GGTCACAGG 2


RESULT 121
BD240651/c
LOCUS       BD240651                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240651
VERSION     BD240651.1  GI:33050421
KEYWORDS    JP 2002534056-A/2069.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 2069 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/2069
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGAT 18
              || ||||||
Db          9 CAGATGGAT 1


RESULT 122
BD248505/c
LOCUS       BD248505                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  T cells specific for target antigens and methods and vaccines based
            thereon.
ACCESSION   BD248505
VERSION     BD248505.1  GI:33058275
KEYWORDS    JP 2002529082-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zauderer,M.
  TITLE     T cells specific for target antigens and methods and vaccines based
            thereon
  JOURNAL   Patent: JP 2002529082-A 19 10-SEP-2002;
            UNIVERSITY OF ROCHESTER
COMMENT     OS   Artificial Sequence
            PN   JP 2002529082-A/19
            PD   10-SEP-2002
            PF   10-NOV-1998 JP 2000581183
            PI   MAURICE ZAUDERER
            PC   C12N15/09,A01K67/027,A61K35/76,A61K39/00,A61K39/04,A61K39/12,
            PC   A61K39/395,
            PC   A61K39/395,A61P31/04,A61P31/10,A61P31/12,A61P35/00,C12N5/10,
            PC   C12Q1/02,
            PC   G01N33/574,C12N15/00,C12N5/00
            CC   Ldd1
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 123
CQ766664/c
LOCUS       CQ766664                  10 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 20 from Patent WO2004005541.
ACCESSION   CQ766664
VERSION     CQ766664.1  GI:44908894
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.
  TITLE     Diagnostic tests for the detection of peripheral neuropathy
  JOURNAL   Patent: WO 2004005541-A 20 15-JAN-2004;
            Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="5-intron/exon, exon 1, gene ABTB1"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              | |||||||
Db         10 CCCATGGTC 2


RESULT 124
CQ858078/c
LOCUS       CQ858078                  10 bp    DNA     linear   PAT 31-AUG-2004
DEFINITION  Sequence 137 from Patent WO2004069189.
ACCESSION   CQ858078
VERSION     CQ858078.1  GI:51852183
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Branch,R.A. and Romkes,M.
  TITLE     Methods of assessment of drug metabolizing enzymes
  JOURNAL   Patent: WO 2004069189-A 137 19-AUG-2004;
            Innovaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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                /note="Description of Artificial Sequence: Synthetic
                oligonucleotide"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACAT 14
              ||||||| |
Db          9 TGGTCACCT 1


RESULT 125
CS065828
LOCUS       CS065828                  10 bp    DNA     linear   PAT 20-APR-2005
DEFINITION  Sequence 32 from Patent WO2005030259.
ACCESSION   CS065828
VERSION     CS065828.1  GI:62818685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vollmer,J., Krieg,A.M. and Uhlmann,E.
  TITLE     Nucleic acid-lipophilic conjugates
  JOURNAL   Patent: WO 2005030259-A 32 07-APR-2005;
            Coley Pharmaceutical Group, Inc. (US); Coley Pharmaceutical GmbH
            (DE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
     misc_feature    10
                     /note="cholesterol"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||| |||||
Db          2 CATCGATGA 10


RESULT 126
CS065828/c
LOCUS       CS065828                  10 bp    DNA     linear   PAT 20-APR-2005
DEFINITION  Sequence 32 from Patent WO2005030259.
ACCESSION   CS065828
VERSION     CS065828.1  GI:62818685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vollmer,J., Krieg,A.M. and Uhlmann,E.
  TITLE     Nucleic acid-lipophilic conjugates
  JOURNAL   Patent: WO 2005030259-A 32 07-APR-2005;
            Coley Pharmaceutical Group, Inc. (US); Coley Pharmaceutical GmbH
            (DE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
     misc_feature    10
                     /note="cholesterol"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||| |||||
Db          9 CATCGATGA 1


RESULT 127
CS065867
LOCUS       CS065867                  10 bp    DNA     linear   PAT 20-APR-2005
DEFINITION  Sequence 71 from Patent WO2005030259.
ACCESSION   CS065867
VERSION     CS065867.1  GI:62818724
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vollmer,J., Krieg,A.M. and Uhlmann,E.
  TITLE     Nucleic acid-lipophilic conjugates
  JOURNAL   Patent: WO 2005030259-A 71 07-APR-2005;
            Coley Pharmaceutical Group, Inc. (US); Coley Pharmaceutical GmbH
            (DE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
     misc_feature    10
                     /note="cholesterol"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||| |||||
Db          2 CATCGATGA 10


RESULT 128
CS065867/c
LOCUS       CS065867                  10 bp    DNA     linear   PAT 20-APR-2005
DEFINITION  Sequence 71 from Patent WO2005030259.
ACCESSION   CS065867
VERSION     CS065867.1  GI:62818724
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vollmer,J., Krieg,A.M. and Uhlmann,E.
  TITLE     Nucleic acid-lipophilic conjugates
  JOURNAL   Patent: WO 2005030259-A 71 07-APR-2005;
            Coley Pharmaceutical Group, Inc. (US); Coley Pharmaceutical GmbH
            (DE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
     misc_feature    10
                     /note="cholesterol"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||| |||||
Db          9 CATCGATGA 1
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RESULT 129
DD199534
LOCUS       DD199534                  10 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  SECRETED AND CELL SURFACE GENES EXPRESSED IN BENIGN AND MALIGNANT
            COLORECTAL TUMORS.
ACCESSION   DD199534
VERSION     DD199534.1  GI:85649025
KEYWORDS    JP 2005518781-A/16.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Vogelstein,B., Bakkuharutsu,P. and Kinzler,K.W.
  TITLE     SECRETED AND CELL SURFACE GENES EXPRESSED IN BENIGN AND MALIGNANT
            COLORECTAL TUMORS
  JOURNAL   Patent: JP 2005518781-A 16 30-JUN-2005;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Homo sapiens
            PN   JP 2005518781-A/16
            PD   30-JUN-2005
            PF   09-SEP-2002 JP 2003526936
            PR   07-SEP-2001 US    60/317494,30-MAY-2002 US    60/383805 PI
            bert vogelstein,philip bakkuharutsu,kenneth w kinzler CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              || ||||||
Db          1 CTTATGGTC 9


RESULT 130
DD199713
LOCUS       DD199713                  10 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  SECRETED AND CELL SURFACE GENES EXPRESSED IN BENIGN AND MALIGNANT
            COLORECTAL TUMORS.
ACCESSION   DD199713
VERSION     DD199713.1  GI:85649600
KEYWORDS    JP 2005518781-A/195.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Vogelstein,B., Bakkuharutsu,P. and Kinzler,K.W.
  TITLE     SECRETED AND CELL SURFACE GENES EXPRESSED IN BENIGN AND MALIGNANT
            COLORECTAL TUMORS
  JOURNAL   Patent: JP 2005518781-A 195 30-JUN-2005;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Homo sapiens
            PN   JP 2005518781-A/195
            PD   30-JUN-2005
            PF   09-SEP-2002 JP 2003526936
            PR   07-SEP-2001 US    60/317494,30-MAY-2002 US    60/383805 PI
            bert vogelstein,philip bakkuharutsu,kenneth w kinzler CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              || ||||||
Db          1 CTTATGGTC 9


RESULT 131
E34261/c
LOCUS       E34261                    10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34261
VERSION     E34261.1  GI:18624266
KEYWORDS    JP 2000106879-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 5 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/5
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATG 15
              ||||| |||
Db          9 GGTCATATG 1


RESULT 132
E39479/c
LOCUS       E39479                    10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genes with human dendritic cell expression.
ACCESSION   E39479
VERSION     E39479.1  GI:18621570
KEYWORDS    JP 2000279181-A/12.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
  TITLE     Genes with human dendritic cell expression
  JOURNAL   Patent: JP 2000279181-A 12 10-OCT-2000;
            SCIENCE & TECH AGENCY
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COMMENT     OS   Homo sapiens (human)
            PN   JP 2000279181-A/12
            PD   10-OCT-2000
            PF   01-APR-1999 JP 1999095481
            PR
            PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 133
E53843/c
LOCUS       E53843                    10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION   E53843
VERSION     E53843.1  GI:18633613
KEYWORDS    JP 2001078772-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
  TITLE     LUNX gene and method for detecting micrometastasis of cancer
  JOURNAL   Patent: JP 2001078772-A 4 27-MAR-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 2001078772-A/4
            PD   27-MAR-2001
            PF   07-SEP-1999 JP 1999253186
            PR
            PI   MORITO KADOTA,YOSHIYUKI FUJIWARA,RYUJI WATANABE,KOICHI OZAKI
            PC   C12N15/09,C07K14/82,C07K16/32,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC
            A61K35/12,A61K35/76,
            PC   A61K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,
            PC   C12N15/00,
            PC   C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 134
AR222953/c
LOCUS       AR222953                  10 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 6 from patent US 6432640.
ACCESSION   AR222953
VERSION     AR222953.1  GI:23330791
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Polyak,K., Vogelstein,B. and Kinzler,K.W.
  TITLE     P53-induced apoptosis
  JOURNAL   Patent: US 6432640-A 6 13-AUG-2002;
            The Johns Hopkins University; Baltimore, MD;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 135
AR282502/c
LOCUS       AR282502                  10 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6521601.
ACCESSION   AR282502
VERSION     AR282502.1  GI:29718976
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Carman,M.D.
  TITLE     Method and composition for inhibition of viral replication
  JOURNAL   Patent: US 6521601-A 9 18-FEB-2003;
            Signal Pharmaceuticals, Inc.; San Diego, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATG 15
              |||||| ||
Db          9 GGTCACGTG 1


RESULT 136
AR303309
LOCUS       AR303309                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 34 from patent US 6544736.
ACCESSION   AR303309
VERSION     AR303309.1  GI:31692085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
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  JOURNAL   Patent: US 6544736-A 34 08-APR-2003;
            Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.;
            Tokyo;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATG 19
              ||| |||||
Db          2 ACAAGGATG 10


RESULT 137
AR303393
LOCUS       AR303393                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 118 from patent US 6544736.
ACCESSION   AR303393
VERSION     AR303393.1  GI:31692169
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 118 08-APR-2003;
            Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.;
            Tokyo;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              || ||||||
Db          2 CAAGGTCAC 10


RESULT 138
AR303484/c
LOCUS       AR303484                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 209 from patent US 6544736.
ACCESSION   AR303484
VERSION     AR303484.1  GI:31692260
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 209 08-APR-2003;
            Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.;
            Tokyo;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATG 19
              ||| |||||
Db          9 ACAAGGATG 1


RESULT 139
AR310652
LOCUS       AR310652                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 16 from patent US 6559125.
ACCESSION   AR310652
VERSION     AR310652.1  GI:31703755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Dervan,P.B., Wurtz,N. and Chang,A.
  TITLE     Polyamide-alkylator conjugates and related products and method
  JOURNAL   Patent: US 6559125-A 16 06-MAY-2003;
            California Institute of Technology; Pasadena, CA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACA 13
              ||||||| |
Db          1 ATGGTCATA 9


RESULT 140
AR364134
LOCUS       AR364134                  10 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 14 from patent US 5256545.
ACCESSION   AR364134
VERSION     AR364134.1  GI:34426460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Brown,M.S., Goldstein,J.L., Russell,D.W. and Sudhof,T.C.
  TITLE     Sterol Regulatory Elements
  JOURNAL   Patent: US 5256545-A 14 26-OCT-1993;
            Board of Regents, The University of Texas System; Austin, TX
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              |||| ||||
Db          1 CATGCATGA 9


RESULT 141
AR442081/c
LOCUS       AR442081                  10 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 53 from patent US 6670119.
ACCESSION   AR442081
VERSION     AR442081.1  GI:42669332
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Yoshikawa,Y., Mukai,H., Asada,K., Hino,F. and Kato,I.
  TITLE     Cancer-associated genes
  JOURNAL   Patent: US 6670119-A 53 30-DEC-2003;
            Takara Shuzo Co., Ltd.; Kyoto;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 142
AR487048/c
LOCUS       AR487048                  10 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 22 from patent US 6706477.
ACCESSION   AR487048
VERSION     AR487048.1  GI:47251995
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zauderer,M.
  TITLE     Methods for producing polynucleotide libraries in vaccinia virus
  JOURNAL   Patent: US 6706477-A 22 16-MAR-2004;
            University of Rochester; Rochester, NY
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 143
AR585253/c
LOCUS       AR585253                  10 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 22 from patent US 6800442.
ACCESSION   AR585253
VERSION     AR585253.1  GI:56629052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zauderer,M.
  TITLE     Methods of selecting polynucleotides encoding antigens
  JOURNAL   Patent: US 6800442-A 22 05-OCT-2004;
            University of Rochester; Rochester, NY
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 144
AR647999/c
LOCUS       AR647999                  10 bp    mRNA    linear   PAT 20-APR-2005
DEFINITION  Sequence 22 from patent US 6872518.
ACCESSION   AR647999
VERSION     AR647999.1  GI:62787239
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zauderer,M.
  TITLE     Methods for selecting polynucleotides encoding T cell epitopes
  JOURNAL   Patent: US 6872518-A 22 29-MAR-2005;
            University of Rochester; Rochester, NY
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               ||||||| |
Db          10 CATGGATCA 2


RESULT 145
AR696636
LOCUS       AR696636                  10 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 16 from patent US 6916610.
ACCESSION   AR696636
VERSION     AR696636.1  GI:75199750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Wang,S.M., Chen,J.-j. and Rowley,J.D.
  TITLE     Method for generation of longer cDNA fragments from sage tags for
            gene identification
  JOURNAL   Patent: US 6916610-A 16 12-JUL-2005;
            Arch Development Corporation; Chicago, IL
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           2 CTCATGGTC 10
               || ||||||
Db           1 CTTATGGTC 9


RESULT 146
AR696640
LOCUS       AR696640                  10 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 20 from patent US 6916610.
ACCESSION   AR696640
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VERSION     AR696640.1  GI:75199755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Wang,S.M., Chen,J.-j. and Rowley,J.D.
  TITLE     Method for generation of longer cDNA fragments from sage tags for
            gene identification
  JOURNAL   Patent: US 6916610-A 20 12-JUL-2005;
            Arch Development Corporation; Chicago, IL
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              || |||||
Db          1 CTTATGGTC 9


RESULT 147
AR778228/c
LOCUS       AR778228                10 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 26 from patent US 6949340.
ACCESSION   AR778228
VERSION     AR778228.1  GI:83356839
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hillis,W.D.
  TITLE     Optical phase modulator
  JOURNAL   Patent: US 6949340-A 26 27-SEP-2005;
            Creative Mines LLC; Bellevue, WA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATG 19
              | |||||||
Db         10 AGATGGATG 2


RESULT 148
AR778232
LOCUS       AR778232                10 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 30 from patent US 6949340.
ACCESSION   AR778232
VERSION     AR778232.1  GI:83356843
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hillis,W.D.
  TITLE     Optical phase modulator
  JOURNAL   Patent: US 6949340-A 30 27-SEP-2005;
            Creative Mines LLC; Bellevue, WA
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATG 19
              | |||||||
Db          1 AGATGGATG 9


RESULT 149
AX021789/c
LOCUS       AX021789                10 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 24 from Patent WO9919476.
ACCESSION   AX021789
VERSION     AX021789.1  GI:10045037
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillespie,L.L. and Paterno,G.D.
  TITLE     Non-mammalian mesoderm induction early response (nm-mier) gene
            family
  JOURNAL   Patent: WO 9919476-A 24 22-APR-1999;
            GILLESPIE LAURA LEE (CA); PATERNO GARY DAVID (CA)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="pcr oligonucleotide"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 150
AX104930
LOCUS       AX104930                10 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1122 from Patent WO0122972.
ACCESSION   AX104930
VERSION     AX104930.1  GI:13921127
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1122 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              |||| ||||
Db          2 CATGTATGA 10
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RESULT 151
AX152753
LOCUS       AX152753                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 668 from Patent WO0138577.
ACCESSION   AX152753
VERSION     AX152753.1  GI:14534404
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 668 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          2 CGTGGTCAC 10


RESULT 152
AX152924/c
LOCUS       AX152924                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 839 from Patent WO0138577.
ACCESSION   AX152924
VERSION     AX152924.1  GI:14534575
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 839 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGAT 18
              || ||||||
Db          9 CAGATGGAT 1


RESULT 153
AX153532/c
LOCUS       AX153532                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1447 from Patent WO0138577.
ACCESSION   AX153532
VERSION     AX153532.1  GI:14535183
KEYWORDS    .
SOURCE      Homo sapiens (human)
 .ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1447 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 154
AX153533/c
LOCUS       AX153533                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1448 from Patent WO0138577.
ACCESSION   AX153533
VERSION     AX153533.1  GI:14535184
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1448 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 155
AX153596/c
LOCUS       AX153596                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1511 from Patent WO0138577.
ACCESSION   AX153596
VERSION     AX153596.1  GI:14535247
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1511 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
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     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 156
AX189798
LOCUS       AX189798                  10 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 16 from Patent WO0148247.
ACCESSION   AX189798
VERSION     AX189798.1  GI:15143169
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Wang,S.M., Chen,J. and Rowley,J.D.
  TITLE     Method for generation of longer cdna fragments from sage tags for
            gene identification
  JOURNAL   Patent: WO 0148247-A 16 05-JUL-2001;
            Arch Development Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              || ||||||
Db          1 CTTATGGTC 9


RESULT 157
AX189802
LOCUS       AX189802                  10 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 20 from Patent WO0148247.
ACCESSION   AX189802
VERSION     AX189802.1  GI:15143173
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Wang,S.M., Chen,J. and Rowley,J.D.
  TITLE     Method for generation of longer cdna fragments from sage tags for
            gene identification
  JOURNAL   Patent: WO 0148247-A 20 05-JUL-2001;
            Arch Development Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTC 10
              || ||||||
Db          1 CTTATGGTC 9


RESULT 158
AX301584/c
LOCUS       AX301584                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 298 from Patent WO0185941.
ACCESSION   AX301584
VERSION     AX301584.1  GI:17382667
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 298 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              | |||||||
Db          9 CGTGGTCAC 1


RESULT 159
AX377141/c
LOCUS       AX377141                  10 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 62 from Patent WO0212561.
ACCESSION   AX377141
VERSION     AX377141.1  GI:19573432
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kazemi,A., Messer,C. and Tanguay,D.A.
  TITLE     Haplotypes of the or1g1 gene
  JOURNAL   Patent: WO 0212561-A 62 14-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACAT 14
              |||||| ||
Db          9 TGGTCAGAT 1


RESULT 160
AX510724/c
LOCUS       AX510724                  10 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 12 from Patent WO0227027.
```

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ACCESSION   AX510724
VERSION     AX510724.1  GI:23391961
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Zauderer,M.
  TITLE     Method of screening for therapeutics for infectious diseases
  JOURNAL   Patent: WO 0227027-A 12 04-APR-2002;
            THE UNIVERSITY OF ROCHESTER (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              ||||||| |
Db         10 CATGGATCA 2


RESULT 161
AX813995
LOCUS       AX813995                  10 bp    DNA     linear   PAT 02-DEC-2003
DEFINITION  Sequence 7 from Patent EP1316605.
ACCESSION   AX813995
VERSION     AX813995.1  GI:38636320
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Aotsuka,S.
  TITLE     Method for producing DNA
  JOURNAL   Patent: EP 1316605-A 7 04-JUN-2003;
            NISSHINBO INDUSTRIES, INC. (JP)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              ||||||| |
Db          2 CATGGTCTC 10


RESULT 162
AX814010
LOCUS       AX814010                  10 bp    DNA     linear   PAT 02-DEC-2003
DEFINITION  Sequence 22 from Patent EP1316605.
ACCESSION   AX814010
VERSION     AX814010.1  GI:38636335
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Aotsuka,S.
  TITLE     Method for producing DNA
  JOURNAL   Patent: EP 1316605-A 22 04-JUN-2003;
            NISSHINBO INDUSTRIES, INC. (JP)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"
     misc_feature    10
                     /note="n=a, g, t or c"

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCAC 12
              ||||||| |
Db          1 CATGGTCTC 9


RESULT 163
AR364134/c
LOCUS       AR364134                  10 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 14 from patent US 5256545.
ACCESSION   AR364134
VERSION     AR364134.1  GI:34426460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Brown,M.S., Goldstein,J.L., Russell,D.W. and Sudhof,T.C.
  TITLE     Sterol Regulatory Elements
  JOURNAL   Patent: US 5256545-A 14 26-OCT-1993;
            Board of Regents, The University of Texas System; Austin, TX
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 80;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CATGGATG 19
              |||| |||
Db          8 CATGCATG 1


Search completed: November 22, 2006, 13:56:08
Job time : 1 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 14:08:15 ; Search time 0.001 Seconds
(without alignments)
27.520 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 38 seqs, 688 residues

Total number of hits satisfying chosen parameters: 76

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 39 summaries

Database : rnpbm.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	US-10-719-370A-446	Sequence 446, App
	2	19	95.0	20	1	US-10-719-370A-141	Sequence 141, App
	3	19	95.0	20	1	US-10-719-370A-447	Sequence 447, App
	4	18	90.0	20	1	US-10-719-370A-445	Sequence 445, App
	5	18	90.0	20	1	US-10-719-370A-452	Sequence 452, App
	6	17	85.0	20	1	US-10-766-185-26	Sequence 26, Appl
	7	17	85.0	20	1	US-10-719-370A-451	Sequence 451, App
	8	16.8	84.0	20	1	US-10-719-370A-443	Sequence 443, App
	9	16	80.0	20	1	US-10-719-370A-448	Sequence 448, App
	10	15.8	79.0	20	1	US-10-719-370A-450	Sequence 450, App
c	11	14.4	72.0	19	1	US-10-310-914A-757115	Sequence 757115,
	12	14.4	72.0	19	1	US-11-083-784-440242	Sequence 440242,
	13	14.4	72.0	19	1	US-11-101-244-440242	Sequence 440242,
c	14	13.8	69.0	19	1	US-11-083-784-15285	Sequence 15285, A
	15	13.8	69.0	19	1	US-11-083-784-144519	Sequence 144519,
	16	13.8	69.0	19	1	US-11-083-784-1218947	Sequence 1218947,
c	17	13.8	69.0	19	1	US-11-101-244-15285	Sequence 15285, A
	18	13.8	69.0	19	1	US-11-101-244-144519	Sequence 144519,
	19	13.8	69.0	19	1	US-11-101-244-1218947	Sequence 1218947,
c	20	13.4	67.0	19	1	US-11-083-784-155627	Sequence 155627,
c	21	13.4	67.0	19	1	US-11-083-784-155645	Sequence 155645,
	22	13.4	67.0	19	1	US-11-083-784-943972	Sequence 943972,
c	23	13.4	67.0	19	1	US-11-083-784-1009396	Sequence 1009396,
	24	13.4	67.0	19	1	US-11-083-784-1224506	Sequence 1224506,
c	25	13.4	67.0	19	1	US-11-101-244-155627	Sequence 155627,
c	26	13.4	67.0	19	1	US-11-101-244-155645	Sequence 155645,
	27	13.4	67.0	19	1	US-11-101-244-943972	Sequence 943972,
c	28	13.4	67.0	19	1	US-11-101-244-1009396	Sequence 1009396,
	29	13.4	67.0	19	1	US-11-101-244-1224506	Sequence 1224506,
c	30	12.2	61.0	17	1	US-09-866-108-7612	Sequence 7612, Ap
c	31	12.2	61.0	17	1	US-10-723-361-7612	Sequence 7612, Ap
	32	11.4	57.0	15	1	US-09-916-466-30	Sequence 30, Appl
	33	11.4	57.0	15	1	US-10-277-494-30	Sequence 30, Appl
c	34	10	50.0	11	1	US-10-949-761-2	Sequence 2, Appli
	35	9.8	49.0	13	1	US-10-257-017B-228161	Sequence 228161,
c	36	9.8	49.0	13	1	US-10-257-017B-228162	Sequence 228162,
	37	9.8	49.0	13	1	US-10-257-017B-245261	Sequence 245261,
c	38	9.8	49.0	13	1	US-10-257-017B-245262	Sequence 245262,
c	39	7.4	37.0	19	1	US-11-083-784-1218947	Sequence 1218947,

ALIGNMENTS

RESULT 1
US-10-719-370A-446
; Sequence 446, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 446
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-446

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCTCATGGTCACATGGATGA 20
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Db          1 CCTCATGGTCACATGGATGA 20
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RESULT 2
US-10-719-370A-141
; Sequence 141, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-141

Query Match 95.0%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCTCATGGTCACATGGATG 19
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Db          2 CCTCATGGTCACATGGATG 20


RESULT 3
US-10-719-370A-447
; Sequence 447, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 447
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-447

  Query Match             95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACATGGATGA 20
              |||||||||||||||||||
Db          1 CTCATGGTCACATGGATGA 19


RESULT 4
US-10-719-370A-445
; Sequence 445, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 445
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-445

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATGA 20
              ||||||||||||||||||
Db          1 TCATGGTCACATGGATGA 18


RESULT 5
US-10-719-370A-452
; Sequence 452, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 452
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (11)..(11)
;   OTHER INFORMATION: n = inosine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (14)..(14)
;   OTHER INFORMATION: n = pseudouridine
US-10-719-370A-452

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 4.5;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              |||||||||| || ||||||
Db          1 CCTCATGGTCNCANGGATGA 20


RESULT 6
US-10-766-185-26
; Sequence 26, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
;  APPLICANT: Yoon, Heejeong
;  APPLICANT:  Ahn, Chang Ho
;  APPLICANT:  Lee, Young  Bok
;  APPLICANT:  Mao, Lingjun
;  APPLICANT:  Jiang, Xiaoming
;  TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
;  FILE REFERENCE: REX 7034
;  CURRENT APPLICATION NUMBER: US/10/766,185
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-26

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGATGA 20
              |||||||||||||||||
```

```
Db          1 CATGGTCACATGGATGA 17


RESULT 7
US-10-719-370A-451
; Sequence 451, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 451
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (12)..(12)
;   OTHER INFORMATION: n = inosine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: n = pseudouridine
US-10-719-370A-451

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 5.8;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              |||||||||| || |||||
Db          2 CCTCATGGTCNCANGGATG 20


RESULT 8
US-10-719-370A-443
; Sequence 443, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 443
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-443

  Query Match             84.0%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 6.1;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              |||||||||| || ||||||
Db          1 CCTCATGGTCGCAGGGATGA 20


RESULT 9
US-10-719-370A-448
; Sequence 448, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-448

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              ||||||||||||||||
Db          5 CCTCATGGTCACATGG 20


RESULT 10
US-10-719-370A-450
; Sequence 450, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 450
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-450

  Query Match             79.0%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 7.9;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              |||||||||| || |||||
Db          2 CCTCATGGTCGCAGGGATG 20
```

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RESULT 11
US-10-310-914A-757115/c
; Sequence 757115, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 757115
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-757115

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 10;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              ||| ||||||||||||
Db         18 CCTGATGGTCACATGG 3


RESULT 12
US-11-083-784-440242
; Sequence 440242, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 440242
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-440242

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 10;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGATGA 20
              | ||:||||:|||:||
Db          4 AAGGUCACAUGGAUGA 19


RESULT 13
US-11-101-244-440242
; Sequence 440242, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 440242
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-440242

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 10;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGATGA 20
              | ||:||||:|||:||
Db          4 AAGGUCACAUGGAUGA 19


RESULT 14
US-11-083-784-15285/c
; Sequence 15285, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 15285
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-15285

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATG 19
              |||||||||  ||||||
Db         18 TCATGGTCAGGTGGATG 2


RESULT 15
US-11-083-784-144519
; Sequence 144519, Application US/11083784
; Publication No. US20050245475A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 144519
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-144519

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 12;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              | :|| ||:||||:|||
Db          2 CAUCAGGGUCACAUGGA 18


RESULT 16
US-11-083-784-1218947
; Sequence 1218947, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1218947
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1218947

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 12;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||:||:||: |||: ||
Db          3 CCUCAUGGUGACAUUGA 19


RESULT 17
US-11-101-244-15285/c
; Sequence 15285, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 15285
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-15285

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATG 19
              |||||||||  ||||||
Db         18 TCATGGTCAGGTGGATG 2


RESULT 18
US-11-101-244-144519
; Sequence 144519, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 144519
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-144519

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 12;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              | :|| ||:||||:|||
Db          2 CAUCAGGGUCACAUGGA 18


RESULT 19
US-11-101-244-1218947
```

```
; Sequence 1218947, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1218947
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1218947

  Query Match            69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity  64.7%;  Pred. No. 12;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||:||:||: |||: ||
Db          3 CCUCAUGGUGACAUUGA 19


RESULT 20
US-11-083-784-155627/c
; Sequence 155627, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155627
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-155627

  Query Match            67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity  93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              |||| ||||||||||
Db         17 TGGTTACATGGATGA 3


RESULT 21
US-11-083-784-155645/c
; Sequence 155645, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155645
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-155645

  Query Match            67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity  93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              |||| ||||||||||
Db         19 TGGTTACATGGATGA 5


RESULT 22
US-11-083-784-943972
; Sequence 943972, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 943972
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-943972

  Query Match            67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity  66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||:| ||:|||:||
Db          5 UGGUCCCAUGGAUGA 19
```

```
RESULT 23
US-11-083-784-1009396/c
; Sequence 1009396, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1009396
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1009396

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATG 15
              ||||| |||||||||
Db         15 CCTCAAGGTCACATG 1


RESULT 24
US-11-083-784-1224506
; Sequence 1224506, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1224506
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1224506

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||: |||:|||:||
Db          2 UGGUUACAUGGAUGA 16


RESULT 25
US-11-101-244-155627/c
; Sequence 155627, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155627
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-155627

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              |||| ||||||||||
Db         17 TGGTTACATGGATGA 3


RESULT 26
US-11-101-244-155645/c
; Sequence 155645, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155645
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-155645

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
```

```
              |||| ||||||||||
Db         19 TGGTTACATGGATGA 5


RESULT 27
US-11-101-244-943972
; Sequence 943972, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 943972
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-943972

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||:| ||:|||:||
Db          5 UGGUCCCAUGGAUGA 19


RESULT 28
US-11-101-244-1009396/c
; Sequence 1009396, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1009396
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1009396

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATG 15
              ||||| |||||||||
Db         15 CCTCAAGGTCACATG 1


RESULT 29
US-11-101-244-1224506
; Sequence 1224506, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1224506
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1224506

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||: |||:|||:||
Db          2 UGGUUACAUGGAUGA 16


RESULT 30
US-09-866-108-7612/c
; Sequence 7612, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
```

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;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7612
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-7612

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 15;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 31
US-10-723-361-7612/c
; Sequence 7612, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7612
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-361-7612

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 15;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 32
US-09-916-466-30
; Sequence 30, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Akhtar, Saghir
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Relatec
;  TITLE OF INVENTION:  Levels of Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-J (400/032)
;  CURRENT APPLICATION NUMBER: US/09/916,466
;  CURRENT FILING DATE:  2001-07-25
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-916-466-30

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 15;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              :||:||:|| |:|
Db          1 UCAUGGUCAAAUG 13


RESULT 33
US-10-277-494-30
; Sequence 30, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Levels
;  TITLE OF INVENTION:  Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-K (400/064)
;  CURRENT APPLICATION NUMBER: US/10/277,494
;  CURRENT FILING DATE:  2002-10-21
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-277-494-30

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 15;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              :||:||:|| |:|
Db          1 UCAUGGUCAAAUG 13


RESULT 34
US-10-949-761-2/c
; Sequence 2, Application US/10949761
; Publication No. US20050266419A1
```

; GENERAL INFORMATION:
; APPLICANT: MGP Biotech, Inc.
; APPLICANT: Pappas, Michael G.
; APPLICANT: Wang, Zhuying
; TITLE OF INVENTION: Apparatus and Method for Detecting Genetic Mutations and Single
; TITLE OF INVENTION: Nucleotide Polymorphisms
; FILE REFERENCE: AL-2004-11
; CURRENT APPLICATION NUMBER: US/10/949,761
; CURRENT FILING DATE: 2004-09-25
; PRIOR APPLICATION NUMBER: 60/509015
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 60/505730
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-10-949-761-2

Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CACATGGATG 19
||||||||||
Db 11 CACATGGATG 2

RESULT 35
US-10-257-017B-228161
; Sequence 228161, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 228161
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055641
US-10-257-017B-228161

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GTCACATGGATGA 20
|| || |||||||
Db 1 GTTACGTGGATGA 13

RESULT 36
US-10-257-017B-228162/c
; Sequence 228162, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 228162
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055641
US-10-257-017B-228162

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GTCACATGGATGA 20
|| || |||||||
Db 13 GTTACGTGGATGA 1

RESULT 37
US-10-257-017B-245261
; Sequence 245261, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 245261
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059887
US-10-257-017B-245261

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGGTCACATGGAT 18
|||| || |||||
Db 1 TGGTAACGTGGAT 13

RESULT 38
US-10-257-017B-245262/c
; Sequence 245262, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 245262

```
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059887
US-10-257-017B-245262

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 18;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGAT 18
              |||| || |||||
Db         13 TGGTAACGTGGAT 1


RESULT 39
US-11-083-784-1218947/c
; Sequence 1218947, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1218947
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1218947

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 47;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATG 19
              |||  |||||   || |
Db         19 TCAATGTCACCATGAGG 3


Search completed: November 22, 2006, 14:08:16
Job time : 1 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 14:11:09 ; Search time 0.001 Seconds
(without alignments)
5.480 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 11 seqs, 137 residues

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 12 summaries

Database : rnpbn.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		19	95.0	20	1	US-11-213-593-186	Sequence 186, App
c 2		10.4	52.0	14	1	US-10-540-460-106	Sequence 106, App
c 3		10.4	52.0	14	1	US-10-540-460-108	Sequence 108, App
c 4		9.4	47.0	11	1	US-11-148-303-357	Sequence 357, App
5		8.4	42.0	12	1	US-11-148-303-258	Sequence 258, App
6		8	40.0	11	1	US-11-364-118-520	Sequence 520, App
c 7		8	40.0	11	1	US-11-148-303-443	Sequence 443, App
c 8		7.8	39.0	11	1	US-11-364-118-535	Sequence 535, App
c 9		7.8	39.0	11	1	US-11-158-209-153	Sequence 153, App
10		7.8	39.0	11	1	US-11-158-209-251	Sequence 251, App
c 11		7.8	39.0	11	1	US-11-158-209-708	Sequence 708, App
c 12		5.6	28.0	20	1	US-11-213-593-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-11-213-593-186
; Sequence 186, Application US/11213593
; Publication No. US20060252720A1
; GENERAL INFORMATION:
; APPLICANT: Eric G. Marcusson
; APPLICANT: Scott Henry
; APPLICANT: Youngsoo Kim
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HIF1-BETA EXPRESSION
; FILE REFERENCE: ISIS-5767/BIOL0046US
; CURRENT APPLICATION NUMBER: US/11/213,593
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US 60/604,190
; PRIOR FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 60/649,586
; PRIOR FILING DATE: 2005-02-02
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 186
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-11-213-593-186

Query Match 95.0%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCTCATGGTCACATGGATG 19
              |||||||||||||||||||
Db          2 CCTCATGGTCACATGGATG 20
```

RESULT 2
US-10-540-460-106/c
; Sequence 106, Application US/10540460
; Publication No. US20060121487A1
; GENERAL INFORMATION:
; APPLICANT: University of Medicine and Dentistry of New Jersey
; APPLICANT: Alland, David
; APPLICANT: Hazbon, Manzour H.
; TITLE OF INVENTION: Method for Single Nucleotide Polymorphism Detection
; FILE REFERENCE: UMD-0019
; CURRENT APPLICATION NUMBER: US/10/540,460
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US 60/437,165
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-540-460-106

Query Match 52.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 TGGTCACATGGA 17
              |||||||||| |
Db         12 TGGTCACATGCA 1
```

RESULT 3
US-10-540-460-108/c
; Sequence 108, Application US/10540460
; Publication No. US20060121487A1
; GENERAL INFORMATION:
; APPLICANT: University of Medicine and Dentistry of New Jersey
; APPLICANT: Alland, David
; APPLICANT: Hazbon, Manzour H.
; TITLE OF INVENTION: Method for Single Nucleotide Polymorphism Detection
; FILE REFERENCE: UMD-0019
; CURRENT APPLICATION NUMBER: US/10/540,460
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US 60/437,165
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:

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;   OTHER INFORMATION: Synthetic
US-10-540-460-108

  Query Match            52.0%;  Score 10.4;  DB 1;  Length 14;
  Best Local Similarity  91.7%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              |||||||||| |
Db         12 TGGTCACATGCA 1


RESULT 4
US-11-148-303-357/c
; Sequence 357, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
;  APPLICANT: Gruenenthal GmbH
;  TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
;  FILE REFERENCE: GR01P003WO
;  CURRENT APPLICATION NUMBER: US/11/148,303
;  CURRENT FILING DATE:  2005-06-09
;  NUMBER OF SEQ ID NOS: 781
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 357
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: V$AP1FJ Q2
US-11-148-303-357

  Query Match            47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity  90.9%;  Pred. No. 4.1;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||| |||||||
Db         11 TCAGGGTCACA 1


RESULT 5
US-11-148-303-258
; Sequence 258, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
;  APPLICANT: Gruenenthal GmbH
;  TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
;  FILE REFERENCE: GR01P003WO
;  CURRENT APPLICATION NUMBER: US/11/148,303
;  CURRENT FILING DATE:  2005-06-09
;  NUMBER OF SEQ ID NOS: 781
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: V$IK2 01
US-11-148-303-258

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity  90.0%;  Pred. No. 5.1;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              |||| |||||
Db          1 CACAGGGATG 10


RESULT 6
US-11-364-118-520
; Sequence 520, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
;  APPLICANT: Olaf Holtkotter
;  APPLICANT:  Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Melanie Giesen
;  APPLICANT:  Daniela Kessler-Becker
;  TITLE OF INVENTION: Method for Determining Hair Cycle Markers
;  FILE REFERENCE: H 06059 PCT
;  CURRENT APPLICATION NUMBER: US/11/364,118
;  CURRENT FILING DATE:  2006-02-28
;  PRIOR APPLICATION NUMBER: PCT/EP2004/009435
;  PRIOR FILING DATE: 2004-08-24
;  PRIOR APPLICATION NUMBER: 103 40 373.6-41
;  PRIOR FILING DATE: 2003-08-30
;  NUMBER OF SEQ ID NOS: 570
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 520
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-364-118-520

  Query Match            40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 6.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ATGGATGA 20
              ||||||||
Db          2 ATGGATGA 9


RESULT 7
US-11-148-303-443/c
; Sequence 443, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
;  APPLICANT: Gruenenthal GmbH
;  TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
;  FILE REFERENCE: GR01P003WO
;  CURRENT APPLICATION NUMBER: US/11/148,303
;  CURRENT FILING DATE:  2005-06-09
;  NUMBER OF SEQ ID NOS: 781
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 443
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: V$AP1FJ Q2
US-11-148-303-443

  Query Match            40.0%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 6.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 ATGGTCAC 12
              ||||||||
Db          9 ATGGTCAC 2


RESULT 8
US-11-364-118-535/c
; Sequence 535, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
;  APPLICANT: Olaf Holtkotter
;  APPLICANT:  Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Melanie Giesen
;  APPLICANT:  Daniela Kessler-Becker
;  TITLE OF INVENTION: Method for Determining Hair Cycle Markers
;  FILE REFERENCE: H 06059 PCT
```

; CURRENT APPLICATION NUMBER: US/11/364,118
; CURRENT FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: PCT/EP2004/009435
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 103 40 373.6-41
; PRIOR FILING DATE: 2003-08-30
; NUMBER OF SEQ ID NOS: 570
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 535
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-364-118-535

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 6.8;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTCATGGTCAC 12
| | |||||||
Db 11 CCCGTGGTCAC 1

RESULT 9
US-11-158-209-153/c
; Sequence 153, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 153
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-153

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 6.8;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGGTCACA 13
||| ||||||
Db 11 TCAGTGTCACA 1

RESULT 10
US-11-158-209-251
; Sequence 251, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 251
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-251

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 6.8;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CATGGTCACAT 14
||| || ||||
Db 1 CATCGTTACAT 11

RESULT 11
US-11-158-209-708/c
; Sequence 708, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 708
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-708

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 6.8;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGGTCACA 13
|| |||| |||
Db 11 TCTTGGTAACA 1

RESULT 12
US-11-213-593-186/c
; Sequence 186, Application US/11213593
; Publication No. US20060252720A1
; GENERAL INFORMATION:
; APPLICANT: Eric G. Marcusson
; APPLICANT: Scott Henry
; APPLICANT: Youngsoo Kim
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HIF1-BETA EXPRESSION
; FILE REFERENCE: ISIS-5767/BIOL0046US
; CURRENT APPLICATION NUMBER: US/11/213,593
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US 60/604,190
; PRIOR FILING DATE: 2004-08-25

; PRIOR APPLICATION NUMBER: US 60/649,586
; PRIOR FILING DATE: 2005-02-02
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 186
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-11-213-593-186

Query Match 28.0%; Score 5.6; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          4 CATGGTCACATG 15
              ||||    ||||
Db         16 CATGTGACCATG 5
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Search completed: November 22, 2006, 14:11:10
Job time : 0.001 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 14:12:47 ; Search time 0.001 Seconds
(without alignments)
0.400 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 10 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5000 summaries

Database : rst.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		7.4	37.0	10	1	CL423977	ACCESSION:CL423977
c 2		3.2	16.0	10	1	CL423977	ACCESSION:CL423977

ALIGNMENTS

RESULT 1
CL423977
LOCUS CL423977 10 bp DNA linear GSS 01-APR-2004
DEFINITION ALE258_TT63-36-1 CSIROPIFGRTT_BDTDNADS_B1 Oryza sativa (japonica cultivar-group) genomic clone RM1065 similar to maps to China Rice GB contig8783, genomic survey sequence.
ACCESSION CL423977
VERSION CL423977.1 GI:45917586
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 10)
AUTHORS Eamens,A.L., Blanchard,C.L., Dennis,E.S. and Upadhyaya,N.M.
TITLE A bidirectional gene trap construct suitable for T-DNA and Ds-mediated insertional mutagenesis in rice (Oryza sativa L.)
JOURNAL Plant Biotechnol. J. 2 (5), 367-380 (2004)
COMMENT Contact: Upadhyaya N.M.
Rice Functional Genomics Group(http://www.pi.csiro.au/fgrttpub/), Genomics and Plant Development Program
CSIRO Plant Industry
Cnr. Barry Drive and Clunies Ross Street, GPO Box 1600; phone 61-2-6246 5491, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5491
Fax: 61 2 6246 5000
Email: narayana.upadhyaya@csiro.au
Flanking sequences were rescued by built-in plasmid rescue system comprising of an ampicillin resistance gene and a bacterial original of replication; First 24 nucleotides are from the respective T-DNA borders (LB or RB) followed by 53 nt filler sequence.
Seq primer: RB specific primer
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .10
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare (Japonica)"
/db_xref="taxon:39947"
/clone="RM1065"
/clone_lib="CSIROPIFGRTT_BDTDNADS_B1"
/note="Vector: Bidirectional gene trapping vector pEU334AN (AY488510) or pEU334BN (AY488511); First 24 nucleotides are from the respective T-DNA borders (LB or RB)."

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          11 ACATGGATG 19
               ||| |||||
Db           2 ACAGGGATG 10
```

RESULT 2
CL423977/c
LOCUS CL423977 10 bp DNA linear GSS 01-APR-2004
DEFINITION ALE258_TT63-36-1 CSIROPIFGRTT_BDTDNADS_B1 Oryza sativa (japonica cultivar-group) genomic clone RM1065 similar to maps to China Rice GB contig8783, genomic survey sequence.
ACCESSION CL423977
VERSION CL423977.1 GI:45917586
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 10)
AUTHORS Eamens,A.L., Blanchard,C.L., Dennis,E.S. and Upadhyaya,N.M.
TITLE A bidirectional gene trap construct suitable for T-DNA and Ds-mediated insertional mutagenesis in rice (Oryza sativa L.)
JOURNAL Plant Biotechnol. J. 2 (5), 367-380 (2004)
COMMENT Contact: Upadhyaya N.M.
Rice Functional Genomics Group(http://www.pi.csiro.au/fgrttpub/), Genomics and Plant Development Program
CSIRO Plant Industry
Cnr. Barry Drive and Clunies Ross Street, GPO Box 1600; phone 61-2-6246 5491, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5491
Fax: 61 2 6246 5000
Email: narayana.upadhyaya@csiro.au
Flanking sequences were rescued by built-in plasmid rescue system comprising of an ampicillin resistance gene and a bacterial original of replication; First 24 nucleotides are from the respective T-DNA borders (LB or RB) followed by 53 nt filler sequence.
Seq primer: RB specific primer
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .10
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare (Japonica)"
/db_xref="taxon:39947"
/clone="RM1065"
/clone_lib="CSIROPIFGRTT_BDTDNADS_B1"

/note="Vector: Bidirectional gene trapping vector pEU334AN (AY488510) or pEU334BN (AY488511); First 24 nucleotides are from the respective T-DNA borders (LB or RB)."

Query Match 16.0%; Score 3.2; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy         12 CATGGATG 19
               |||   ||
Db         10 CATCCCTG 3
```

Search completed: November 22, 2006, 14:12:47
Job time : 0.001 secs